

**THE ROLE OF TREFOIL FACTOR 3
IN MAMMARY CARCINOMA ANGIOGENESIS**

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DECLARATION

I hereby declare that this thesis is my original work and it has been written by me in its entirety. I have duly acknowledged all the sources of information which have been used in the thesis.

This thesis has also not been submitted for any degree in any university previously



Lau Wai Hoe
22 August 2014

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Summary

Angiogenesis is associated with metastasis of mammary carcinoma. Angiogenesis occurs in response to the stimulation of angiogenic factors secreted by mammary carcinoma or stromal cells (Folkman *et al.*, 1971, Folkman, 1992). Trefoil Factor 3 (TFF3) is a small secreted protein and physiologically involved in mucosal repair and restitution (Taupin and Podolsky, 2003). Increased TFF3 expression is oncogenic and stimulates invasiveness and metastasis of mammary carcinoma cells (Kannan *et al.*, 2010, Pandey *et al.*, 2014).

The role of TFF3 in *de novo* angiogenesis of mammary carcinoma has not been determined. Herein, I defined the effect of TFF3 secreted from mammary carcinoma cells on human umbilical vein endothelial cells (HUVEC) using an indirect co-culture transwell system in which mammary carcinoma cells were plated in the membrane of transwell insert co-cultured with HUVEC seeded in the bottom well of companion plate. Forced expression of TFF3 in mammary carcinoma cells promoted HUVEC monolayer proliferation, cell cycle progression, survival, migration, invasion, and tubule formation *in vitro*. In xenograft models, mammary carcinoma cells with forced expression of TFF3 produced tumors with increased IL-8 expression and enhanced microvessel density (CD31 and CD34 positive) as compared to tumors formed by control cells. Depletion of TFF3 in mammary carcinoma cells by siRNA decreased the angiogenic behaviors of HUVEC. Mechanistically, forced expression of TFF3 in mammary carcinoma cells stimulated IL-8 promoter activity and subsequently increased IL-8 expression. Depletion of IL-8 in mammary carcinoma cells by siRNA or inhibition of IL-8 with anti-IL-8 monoclonal antibody abrogated the stability of TFF3 on stimulation of HUVEC migration, invasion, and tubule formation *in vitro*. Blocking of IL-8 receptor namely CXCR2 in HUVEC by anti-CXCR2 monoclonal antibody inhibited TFF3-stimulated HUVEC tubule formation *in vitro* mediated by IL-8. TFF3 enhanced STAT3 phosphorylation. Depletion of STAT3 in mammary carcinoma cells by siRNA partially abrogated the effect of TFF3 on IL-8 promoter activity and subsequently decreased IL-8 expression. Depletion of STAT3 in mammary carcinoma cells by siRNA also partially abrogated the stimulatory

effects of TFF3 on HUVEC migration, invasion and tubule formation *in vitro*. Furthermore, exogenous rhTFF3 stimulated HUVEC monolayer proliferation, migration, invasion, and tubule formation *in vitro* in a concentration-dependent manner. Exogenous rhTFF3 directly acted on HUVEC to promote angiogenic behaviors of HUVEC. Additionally, TFF3 secreted from HUVEC increased monolayer cell proliferation, cell cycle progression, survival, migration, invasion, and tubule formation *in vitro*. TFF3 secreted from HUVEC enhanced IL-8 promoter activity and increased IL-8 expression in endothelial cells, albeit slightly. Hence, TFF3 is a promoter of angiogenesis, which may co-coordinate with the growth promoting and metastatic actions of TFF3 in mammary carcinoma to enhance tumor progression.

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List of Abbreviations

ADH: Atypical hyperplasia
ANGPT1: Angiopoietin 1
ANGPT2: Angiopoietin 2
BrdU: 5-bromo-2-deoxyuridine
CAF: Cancer Associated Fibroblast
CAM: Chorioallantoic membrane
CNS: Central Nervous System
COL18A1: Collagen alpha-1(XVIII) chain
c-Src: Cellular sarcoma
DCIS: Ductal Carcinoma *In situ*
EC: Endothelial Cells
ECM: Extracellular Matrix
EGF: Epidermal Growth Factor
EGFR: Epidermal Growth Factor Receptor
EMT: Epithelial Mesenchymal Transition
ER: Estrogen Receptor
GI tract: Gastrointestinal tract
GH: Growth Hormone
HER-2/neu: Human Epithelial Receptor 2
hGH: human Growth Hormone
hSIE: human sis-inducible element
HIF: Hypoxia Inducible Factor
hTERT: human Telomerase Reverse Transcriptase
HUVEC: Human Umbilical Vein Endothelial Cell
IBC: Invasive Breast Cancer
IDC: Invasive Ductal Carcinoma
IGF-1: Insulin Growth Factor 1
ILC: Invasive Lobular Carcinoma
LCIS: Lobular Carcinoma *In situ*
MMP: matrix metalloproteinases
NFκB: Nuclear factor kappa B
PDGF: Platelet-Derived Growth Factor
PR: Progesterone Receptor
PI3K: Phosphoinositide 3-kinases
PIGF: Placental Growth Factor
PG: Progesterone
SAGA: Serial Analysis of Gene Expression
STAT: Signal Transducer and Activating of Transcription
TEK: Angiopoietin-1 receptor
TFF: Trefoil Factor
TGFB: Transforming Growth factor beta
TME: Tumor microenvironment
TKI: Tyrosine Kinase Inhibitor
TNF: Tumor necrosis factor
Tsp: Thrombospondin
VBM: Vascular basement membrane
VEGF-A: Vascular Endothelial Growth Factor-A
VEGFR: Vascular Endothelial Growth Factor Receptor

CHAPTER 1

Introduction

Trefoil factors (TFF) family consists of three members, namely TFF1, TFF2, and TFF3. In the normal physiology, all three TFF proteins are expressed in the epithelial cells that line the mucous membrane. The biological functions of TFF peptides include protection of gastrointestinal (GI) tract from injury and mucosal restitution (Taupin *et al.*, 2000b, Taupin and Podolsky, 2003). However, TFF peptides, particularly Trefoil factor 3 (TFF3) have been documented to be over-expressed in human malignancies including breast (Poulsom *et al.*, 1997), gastric (Yamachika *et al.*, 2002, Dhar *et al.*, 2005), prostate (Faith *et al.*, 2004), hepatocellular (Okada *et al.*, 2005), and endometrial (Bignotti *et al.*, 2008). Accumulating evidence suggests that increased expression of TFF peptides is tightly linked to the progression of cancers (May and Westley, 1997a). This introduction will be divided into five sections. The first section describes hallmarks and the development of cancer. The second sections describes pathogenesis and treatment of human mammary carcinoma. The third section describes the biology of TFF3, the signaling pathways of TFF3, and the potential oncogenic effects of TFF3 in cancer progression. The fourth section describes the mechanism and regulation of angiogenesis, and the angiogenic factors involved in tumor angiogenesis. The last section describes the rationales and objectives of this research project.

1.1 Epidemiology of cancer

Cancer is a major disease worldwide with an annual incidence of greater than 10 million (Stewart *et al.*, 2003). In 2012, the newly diagnosed cancer cases and cancer death were approximately 14.1 million and 8.2 million respectively (Ferlay *et al.*, 2012). Cancer is the second commonest of death that accounts with nearly 25% of all deaths. In 2014, the number of newly diagnosed cancer cases is expected to be approximately 1.7 million with cancer deaths of 585,720 in the United States (American Cancer Society, 2014). Current

statistics indicate that 50% of men and 30% of women will develop cancer during their lifetime (Howlader *et al.*, 2014). According to the American Cancer Society, the leading cancer death for men (28%) and women (26%) is lung cancer, followed by prostate (10%) in men and breast (15%) in women (American Cancer Society, 2014). The mortality rate showed only a slight decline, despite advances in early diagnosis and introduction of new therapeutic modalities tailored to target cancer cells. The statistics underlie the importance of understanding the biology of cancer and its signaling pathway.

1.1.1 Heterogeneity of cancer

Cancer is a neoplastic disease characterized by alterations of the genome that results in deregulation of normal cell processes including cell division and cell differentiation. Consequently, the normal balance between the cell replication and cell death is disturbed, thereby, resulting in uncontrolled cell proliferation (Vogelstein and Kinzler, 2004, Ruddon, 2007). Under normal physiological conditions, normal cells divide in response to growth factor signals cease dividing in response to anti-growth signals (Vogelstein and Kinzler, 2004, Ruddon, 2007). The signaling molecules that moderate cell division are released by neighboring cells. In response to genetic or environmental insults, normal cells undergo programmed cell death or apoptosis. Cancer is a genetic disease that originates from a single ancestral cell and is clonal in nature. Tumors starts when a single cell acquires a series of mutations which collectively transforms normal cells into cancerous cells that divide uncontrollably and eventually spread throughout the body (Hanahan and Weinberg, 2000). As cancer growth progresses, genetic drift such as gene alteration or mutation produces heterogeneity in cancer cell population (Futreal *et al.*, 2004). Tumors are classified as either benign or malignant. Benign tumors are non-cancerous cells that unable to invade neighboring tissues or metastasize, and can only grow locally. Malignant tumors are cancer cells that are able to invade, spread to lymph nodes or bloodstream, and metastasize to secondary site in the body (Silverstein *et al.*, 2006). In general, malignant tumors cause

significant morbidity and are fatal if untreated. The etiology of cancer is complex, and partially understood. Current studies indicated that only 5 - 10% of cancer is attributed to genetic defects and the remaining is caused by environmental and lifestyle factors (Anand *et al.*, 2008, Khan *et al.*, 2010), suggesting that cancer is a preventable disease and could be treated if it is detected early with therapeutic treatments.

1.1.2 The hallmarks of cancer

Cancer is a complex and multifactorial disease in which there is strong interplay between genetic and environmental factors. Perturbations of the normal control mechanism drive normal cells to become cancerous cells. Cancer cells acquire a series of genetic mutations that lead to uncontrolled cell growth and division, inhibition of cell differentiation, and resistance to cell death (Futreal *et al.*, 2004). Tumors secrete angiogenic factors that stimulate new blood vessels formation in a process known as angiogenesis to supply cancer cells with oxygen and nutrients, a process called angiogenesis (Folkman, 1990). Some malignant tumors may remain localized and encapsulated. However, most cancer cells eventually invade surrounding tissue and breaking through the basal laminas to spread to distant organs in a process called metastasis (Varmus and Weinberg, 1993). The ability of cancer cells to override normal control mechanisms is underlined by six "hallmarks of cancer" as proposed by Hanahan and Weinberg (2000). The hallmarks of cancer encompass six biological features acquired during cancer cells development. The acquired biological capabilities are as follows (Figure 1):

(i) Self-sufficiency in growth signal.

The ability of cancer cells to divide without growth factor stimulation. Deregulation of cell surface receptors (i.e. growth factor receptors) that rely on growth-stimulatory signals into the cells during tumor pathogenesis and receptors over-expression may also enable the cancer cells to become hyper-responsiveness to growth factors (Fedi *et al.*, 2000). Mutation or structural alterations in cell surface receptors resulted in ligand independent growth signaling

pathways or cross-talking connections with other pathways to trigger multiple biological effects.

(ii) Insensitivity to anti-growth signals.

In cancer, cells acquire the ability to divide in the presence of anti-growth signals. On the contrary, under normal cellular condition, anti-growth signals can inhibit proliferation by forcing actively proliferating cells to enter quiescent (G_0) state. Alternatively, cells may be induced to enter into postmitotic state resulting in inhibition of their proliferative potential. However, cancer cells evade anti-growth signals by avoiding differentiation and promoting growth.

(iii) Evading apoptosis.

Cancer cells acquired capability to escape apoptosis or programmed cell death. The growth of tumor cell is influenced by both the rate of cell proliferation as well as the rate of apoptosis. Acquiring the capability to resist apoptosis can be through a variety of strategies such as mutation in p53 tumor suppressor gene and loss of function of a pro-apoptotic regulator, which resulting in production of functional inactivation of p53 protein (Harris, 1996). An estimated of more than 50% of cancers contained p53 mutations that results in promoting survival signaling pathway instead of apoptotic machinery.

(iv) Limitless replication potential.

Cancer cells acquired capability for unlimited replication and maintenance of telomere length despite repeated cell divisions. Normal cells have a limited number of doublings to be completed before entering senescence (aging process) (Hayflick, 1997). However, cancer cells acquired the capability to multiply without limit and attribute an infinite replicative potential, the trait termed as immortalization, i.e. the ability of a cell to continue dividing without limit. Telomeres are eroded with every cell cycle and the erosion signals a cell to enter senescence. Hence, maintenance of telomerase is observed in 85 - 90% of all type of cancer cells through up-regulation of telomerase enzyme expression or elevating telomerase activity (Shay and Bacchetti, 1997).

(v) Sustained angiogenesis.

Angiogenesis is a cellular event whereby new blood vessels are formed to supply oxygen and nutrients to tissues. It is a tightly regulated process, which becomes deregulated in cancer, whereby neoplastic lesions stimulate sprouting of pre-existing blood vessels or formation of new vasculatures to facilitate tumor growth and metastasis (Bouck *et al.*, 1996, Hanahan and Folkman, 1996).

(vi) Tissue invasion and metastasis.

As cancer progresses, cells acquire capability that enables invasion into surrounding tissues and subsequent dissemination to other parts of the body. The main cause of cancer deaths is due to the metastasis where primary tumor spread to the other parts of the body (Sporn, 1996). Metastasis is a complex mechanism involving dissolution of cell-to-cell contacts (e.g., down-regulation of adhesion proteins such as E-cadherin), alteration of cell-to-microenvironment interactions in cancer through changes in integrin expression, and activation of extracellular proteases and matrix degrading proteases responsible for degrading extracellular matrix (ECM) substrates in cancer cells (Coussens and Werb, 1996, Christofori and Semb, 1999). The capability for cancer cells to invade and metastasize enables escape from the primary tumor site and colonizes at distant organs with sufficient supply of nutrient and growth factors.

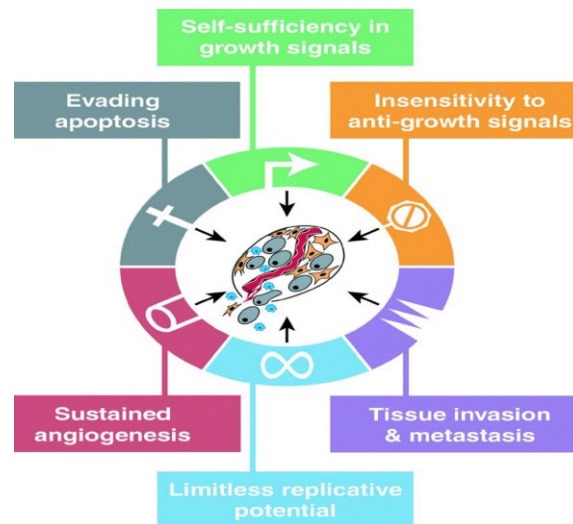


Figure 1: The hallmarks of cancer. The hallmarks of cancer describe functional characteristics, which most cancers acquire during the process of tumor growth and progression (Hanahan and Weinberg, 2000). Reproduced with permission.

The hallmarks of cancer activities are important acquired capabilities that required for development and maintenance of cancer. Further, these acquired capabilities restated that cancer as a multistep disease mainly initiated through the perturbation of the cellular regulatory mechanisms that important for normal cell proliferation as well as homeostasis (Hanahan and Weinberg, 2000). In addition to the existing functional characteristics, genome instability in cancer cells produces genetic variability that accelerates their acquisition of capabilities. Besides, tumor-microenvironment interaction may produce inflammatory responses that are advantages to the cancer cells. The high proliferative state and survival of cancer cells produce genomic instability associated with DNA mutations or DNA damage repair (Charames and Bapat, 2003) and chromosomal abnormalities associated with mutations in oncogenes such as TP53. Consequently, the mechanisms controlling cell cycle, telomere length, and telomerase activity are deregulated (Negrini *et al.*, 2010). Furthermore, two emerging hallmarks have recently been described in the pathogenesis of all if not some cancers (Figure 2). Firstly, deregulating cellular energetics such as modification or reprogramming of metabolism is necessary for cancer cells proliferation. Secondly, avoiding immune destruction provided cancer cells the advantage to escape immunological

surveillance, particularly by lymphocytes and natural killer cells (Hanahan and Weinberg, 2011). Acquisition of these hallmarks lead to the generation of mutant cells with an increased oncogenic potential (Floor *et al.*, 2012).

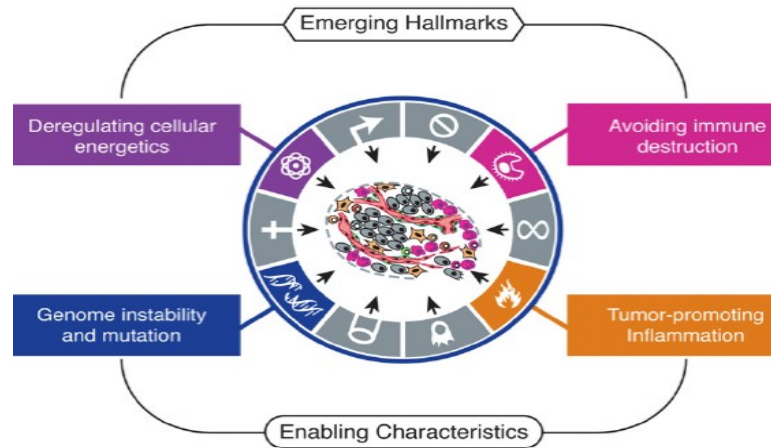


Figure 2: Emerging hallmarks and enabling characteristics. Two additional hallmarks of cancer, namely deregulating cellular energetics and avoiding immune destruction, are implicated in the pathogenesis of cancers. Genomic instability in cancer cells caused by mutations promotes tumor progression. Inflammation initiated by immune cells that function to fight against infections and injury can support multiple hallmark capabilities instead (Hanahan and Weinberg, 2011). Reproduced with permission.

1.1.3 Tumor microenvironment

The highly proliferative cancer cells have been suggested as one of the most crucial agents in the tumor mass. Carcinoma arising from epithelium is initiated by mutation. However, promotion of tumor progression involved the stroma in the tumor environment (Egeblad *et al.*, 2005). Therefore, the series of mutations in cancer cells do not completely elucidate the aggressive or invasive phenotype of tumors (Sager, 1997, Park *et al.*, 2000, Ronnov-Jessen and Bissell, 2009). It was lately discovered that the gene expressions of cells in the tumor microenvironment (TME) is essential for cancer cells to become malignant (Sager, 1997). Emerging evidence indicates that tumorigenesis involve complex heterogeneous interactions between tumors and its interstitium (Liotta and Kohn, 2001, Dvorak *et al.*, 2011). The distinct population of cells that constitute solid tumors include

cancer mesenchymal cells, cancer stem cells, other cell types such as fibroblasts, endothelial cells, stroma cells, and immune inflammatory cells, and the ECM. Together, these components create the tumor microenvironment that contributes to the acquisition of hallmark traits, thereby promoting tumor progression (Hanahan and Weinberg, 2011, Floor *et al.*, 2012).

The capability of the TME to promote tumor growth and progression results from exploiting the ability of its cellular components, particularly cancer-associated fibroblasts, macrophages and endothelial cells (Figure 3). In the immune system, immunological cells play a role to eliminate foreign cellular components such as tumors. However, in cancer, these immunological cells can be paralyzed, which in turn become advantageous for tumor growth and metastasis (Leibovici *et al.*, 2011). The stroma supports tumors growth by providing growth factors from degradation of the extracellular matrix (ECM) by the matrix metalloproteinases (MMPs). Additionally, stroma provides angiogenic factors, which promotes vascularization necessary for growth and metastasis (Leibovici *et al.*, 2011). Therefore, the TME is involved to promote progression of tumor at different stages through the enhancement of invasion, angiogenesis and metastasis (Whiteside, 2008). It has been explicitly shown that tumor microenvironment have a critical part in tumor development and progression (Dvorak *et al.*, 2011).

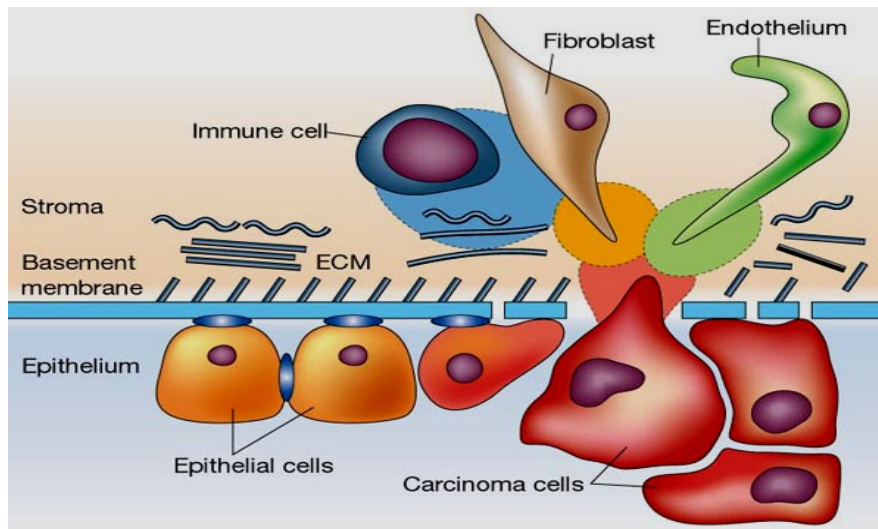


Figure 3: Microenvironment of tumor. The transition from non-invasive to invasive carcinoma required activation of a range of cell types including fibroblasts, immune cells and endothelial cells. Interaction between the stromal cells and the premalignant epithelium is needed for invasion (Liotta and Kohn, 2001). Reproduced with permission.

1.1.4 Invasion metastasis cascade

At advanced stages of primary tumors, cancer cells can gain entry into blood or lymphatic vessels, circulate through the intravascular stream, and proliferate at distant site in the body in a process known as metastasis. The multistep process of cell-biological events has been schematized as sequential and interrelated steps, defined as invasion-metastasis cascade (Fidler, 2003, Talmadge and Fidler, 2010). Each step of this cascade is important as failure to complete any step effectively impedes the tumor cells success to invade and metastasize (Poste and Fidler, 1980). During the process of invasion and metastasis, a series of events have to take place (Figure 4), which begin from local invasion through ECM at primary site, followed by intravasation into blood vessels, survival in circulation, arrest at secondary site, subsequently extravasation into secondary tissues, survival in new microenvironments by forming micrometastases, reinitiation of proliferation, and finally production of macroscopic tumors (referred to “metastatic colonization”) (Fidler, 2003, Hanahan and Weinberg, 2011).

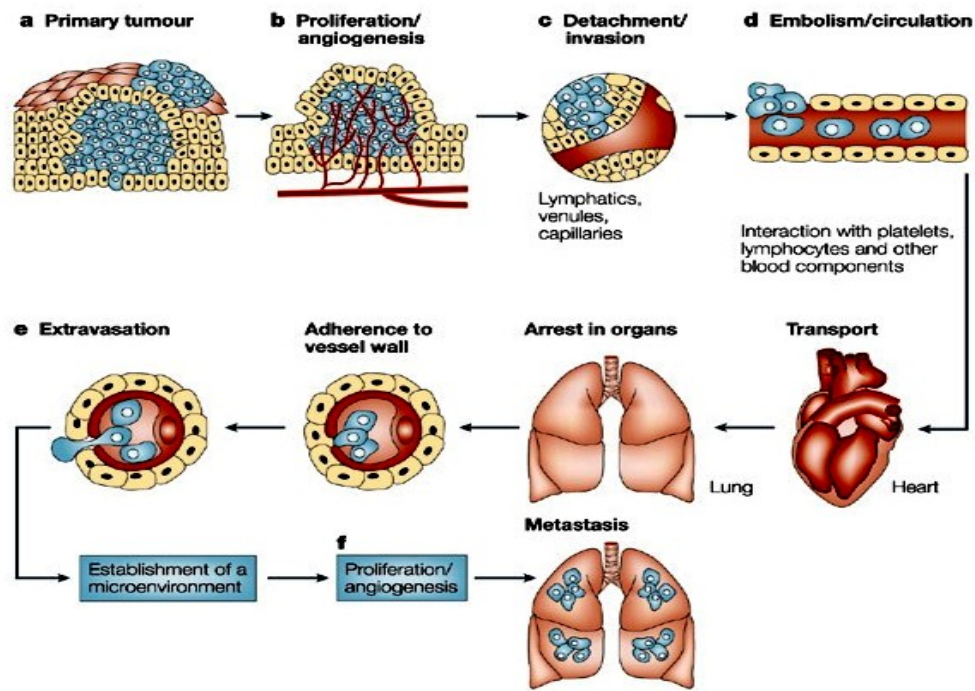


Figure 4: The invasion-metastasis cascade. Invasion-metastasis is a complex series of cellular events. During metastatic progression, cancer cells invade locally from the primary tumor site, break through the basement membrane, enter into the circulation, arrest at a secondary site, and survive in the secondary tissues (Fidler, 2003). Reproduced with permission.

Accumulating evidence have shown that the normal tissue architecture serves as barrier against invasion which cancer cells have to break through to metastasize successfully (Valastyan and Weinberg). The ECM in tissue architecture provides a support for organization of cells into specific tissues. For example, basement membrane of the ECM structures served as physical barrier that prevents invasion and metastasis. To initiate the invasion-metastasis cascade, cell invasion initially participated in modification of cell adhesion, degradation of ECM, and migration of tumor cells. Subsequently, the cancer cells could co-opt with epithelial-mesenchymal transition (EMT) program that implicated in normal embryonic morphogenesis (Shook and Keller, 2003). Epithelial cells are connected with each other by cell-cell junctions to ensure the integrity and the stabilization of the epithelium. During the process of EMT, the tumor cells acquire invasion and migration characteristics, thereby promoting the cancer cells migrate through the ECM (Figure 5).

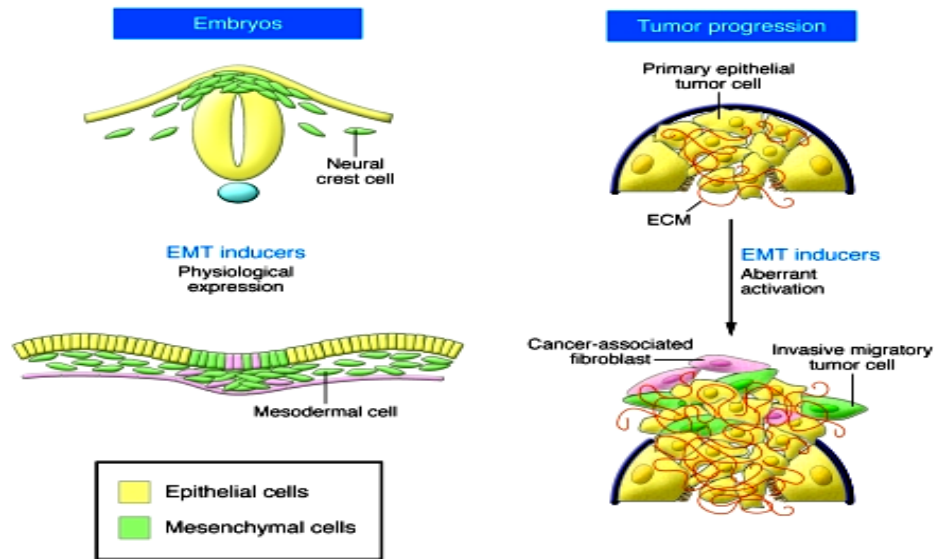


Figure 5: EMT in development and disease. In normal conditions, EMT (cells in green) occurs during development of embryos, such as during neural crest cell delamination from the dorsal neural tube. EMT inducers usually remained quiescent but become highly active in invasive carcinomas. The influence of cell state during development or disease is highly dependent on epithelial-mesenchymal transitions (Acloque *et al.*, 2009). Reproduced with permission.

EMT inducers are activated in primary tumor which lead to the dissociation of adherens or tight junctions, loss of cell polarity, transition of epithelial cell to adopt mesenchymal characteristics which include increased cellular invasiveness and aggressiveness (Baum *et al.*, 2008, Thiery *et al.*, 2009) (Figure 6). Furthermore, EMT is organized by a set of transcription factors, including ZEB1, SLUG, TWIST, SNAIL, and ZEB2 that allows carcinoma cells to gain mesenchymal properties by repressing expression of epithelial markers and inducing expression of mesenchymal markers (Thiery *et al.*, 2009).

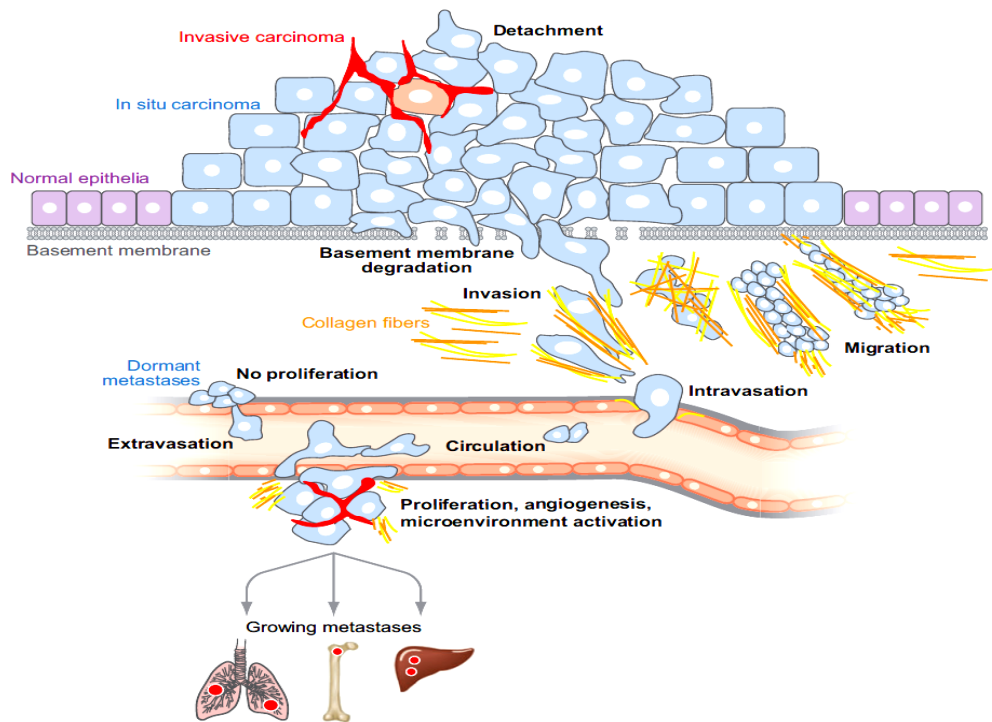


Figure 6: Cellular events in EMT. The EMT occurs at the primary tumor site whereby normal epithelial cells transform into invasive carcinoma *in situ* due to the loss of tight/adherents junctions as well as cell polarity. As basement membrane becomes degraded, tumor cells begin to invade the surrounding stroma to intravasate into blood vessels or lymph node, and finally be transported in circulation until they colonize at a distant organ (Bacac and Stamenkovic, 2008). Reproduced with permission.

EMT is induced by multiple signaling pathways that mediated by growth factors, Src, Ras, Integrin, Wnt/beta-catenin and Notch. One of the most important molecular characteristic of EMT is the down-regulation of E-cadherin, which is a cell adhesion molecule commonly found in normal epithelial cells and plays a role in tumor suppression. However, the expression of E-cadherin is found to be down-regulated during cell transformation (Larue and Bellacosa, 2005). Numerous studies have shown that TGF- β to be a multifunctional peptide can suppress or promote tumors formation (Muraoka-Cook *et al.*, 2005, Lebrun, 2012). The TGF- β pathway is found to suppress cell transformation by preventing cell division and inducing cell death or senescence. During late tumorigenesis, stimulation of TGF- β signaling is associated with cancer-related events such as promoting cell proliferation, cell motility, new blood vessels development, invasion and metastasis (Muraoka-Cook *et al.*, 2005, Lebrun, 2012). Metastatic events are stimulated by EMT through activation of the

phosphatidylinositol 3' kinase (PI3K)/Akt signaling pathway that induces Slug- or Snail-mediated repression of E-cadherin gene, which in turn resulted in alterations of cell morphology, tumorigenicity, cell motility and invasiveness (Larue and Bellacosa, 2005). TWIST is an EMT transcription factor, which induces EMT and contributes metastatic feature of tumors (Yang *et al.*, 2004). Therefore, multiple signaling pathways determine the growth and metastatic potential of tumors.

1.2 Human mammary carcinoma

Human mammary carcinoma is also known as breast cancer. It is a type of tumor that originates from breast tissue i.e. epithelial cell in the inner lining of milk ducts or the lobules (Sariego, 2010). Benign breast conditions (non-cancerous) are very commonly found in women. Non-invasive or *in situ* breast cancers are malignant breast tumors that remain inside the ducts and have not spread into the surrounding breast tissue (Majure, 2000). This type of breast cancer could be cured by early detection and treatment. In contrast, invasive (infiltrating) breast cancers spread beyond the membrane lining a duct or lobule, invade the neighboring tissue and metastasize to the liver, lung, and brain (Majure, 2000). This type of breast cancer can severely affect the mortality or morbidity of women.

1.2.1 Epidemiology of mammary carcinoma

Mammary carcinoma is the major cause of death for women worldwide that accounts for 29% (232,670) of newly diagnosed cancer cases and 15% (40,000) of total cancer mortality in the United States (American Cancer Society, 2014). It is estimated that about 12.3% women will be diagnosed with breast cancer in their lifetime (Siegel *et al.*, 2014). Moreover, World Health Organization (WHO) predicts that up to 70% of the new breast cancer cases will occur in the developing countries by 2020 (Ferlay *et al.*, 2012) and that 84 million of people will be affected in the next 10 years if no actions are taken (Morabia and Abel, 2006)

In Singapore, cancer is the leading cause of mortality, constituting 18,481 of total cancer deaths and 56,316 new cancer cases in 2012. The incidence rates of cancer have increased for the period 2006 - 2010 (Teo and Soo, 2013). Breast cancer is the top frequently diagnosed cancer (29.4%) with mortality rate of 17.9% in Singapore women (Singapore Cancer Registry, 2012). About 1,600 women are diagnosed with breast cancer each year (Singapore Cancer Registry, 2012). GLOBOCAN 2012 revealed a sharp rise of breast cancer incidence in women and highlighted to the importance and priority of preventive and control measures (Ferlay *et al.*, 2012). There is an urgent demand for eradicating breast cancer, encouraging considerable efforts to elucidate the underlying mechanism of this deadly disease.

1.2.2 Development and structure of normal human mammary gland

The mammary gland is a highly complex, dynamic, and specialized organ that consists of multiple lobes. Each lobes are made up of several lobules that contain multiple acini, which eventually drain milk into the nipple via the ducts (Owens *et al.*, 2013). The basic functional unit in the human mammary gland is terminal end bud (TEB) consists of a lobule and the draining duct supported by a network of adipose tissues and connective tissue (Ramsay *et al.*, 2005). Human mammary gland is composed of glandular structures whose major function is to produce milk under the influence and control of hormones.

Mammary gland development take places at different stages such as embryonic, prepubertal, pubertal, pregnancy, lactation, and involution that are related during reproduction as well as sexual development (Hennighausen and Robinson, 2001). In the embryogenesis of mammary development, both males and females share the same primitive mammary gland at birth. In female, mammary gland development is initiated during the onset of puberty and is regulated by the elevated secretion of ovarian hormones such as estrogen and progesterone. After puberty, the female mammary gland experienced cycles of growth and morphologic changes including TEB formation, ductal elongation, lateral branching, and terminal duct lobular formation as well as stroma expansion. Additionally, morphologic changes to or

regulation of female mammary glands are governed by the menstrual cycle, pregnancy and lactation (Ali and Coombes, 2002). Unlike females, the male mammary glands do not undergo morphologic changes and remained in quiescent state (Sternlicht, 2006). The female mammary gland consist a primitive branching ductal system and the process of duct and acini development is known as branching morphogenesis. The duct originates in the fetus and terminates at early childhood until puberty when hormones begin to stimulate and trigger differentiation. Under hormonal influences, the interaction between epithelium and mesenchyme results in differentiation of the prenatal primitive structure to produce a mature mammary gland (Javed and Lteif, 2013):

Humans have two complex mammary glands that consist of 10 - 20 simple glands in each breast. Two tissue compartments that constitute the mammary gland are the parenchyma, which forms the branching duct system from which secretory acini develop. The mammary fat pad is made up of adipose stroma or connective tissue which serves a support in which the parenchyma develops and functions (Medina, 1996). The parenchyma is composed of the alveoli that are made up of milk-secreting epithelial cells that are surrounded by myoepithelial cells (Figure 7). The branching ductal system is mainly developed during puberty. In contrasts, the lobuloalveolar begins to develop during pregnancy. The ducts branch into smaller ductules that terminate in lobules.

The mammary gland is composed of approximately 15 - 20 lobes. The mammary epithelium is mainly composed of two cell types, the basal and the luminal. The basal epithelium comprises the myoepithelial and a subpopulation of stem cells. The myoepithelial cells possess contractile functions and form the outer layer of the mammary gland. The function of the small subpopulation of stem cells is to generate or produce different cell types. The luminal epithelium gives rise to the ducts and secretory alveoli. Both myoepithelium and luminal epithelium function together to generate a bi-layered, tubular structure that enables contraction of myoepithelial cells to discharge milk during lactation (Macias and Hinck, 2012).

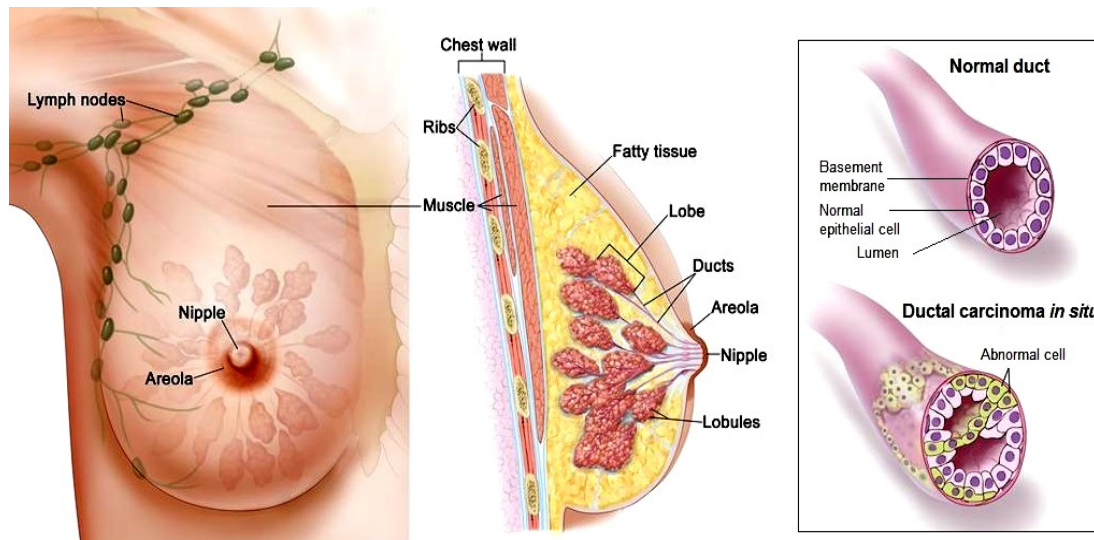


Figure 7: Anatomy of the human mammary gland. Mammary carcinoma duct is covered with a layer of epithelial cells that function in producing milk. The glands are surrounded by an outer layer of myoepithelial cells that possess contractile properties. Abnormal cells are found in ductal carcinoma. Adapted from <http://www.breastcancer.org>.

It has been proposed that the cell lineages that compose the mammary gland are derived from a mammary stem cell population (Smalley and Ashworth, 2003). A hierarchy of stem cells including unipotent and multipotent cells appear to be present within the mammary gland whereby each of them likely to have a distinct function in the morphogenesis and mammary epithelium maintenance (Van Keymeulen *et al.*, 2011). These cells are capable of differentiating into multiple cell type of the mammary gland depending on different stages such as during development, pregnancy or even self-renewal. Self-renewal is essential to drive the growth of subsequent pregnancies due to the massive apoptotic events occurring during post weaning. (Tiede and Kang, 2011). It has been postulated that the mammary stem cells (MSCs) made up the epithelial compartment of the mammary gland. These MSCs possess self-renewal potential and produce epithelial precursor cells, which are further differentiated into either basal or luminal epithelial (Figure 8). The presence of stem cells is the fundamental for renewal of alveolar in each pregnancy.

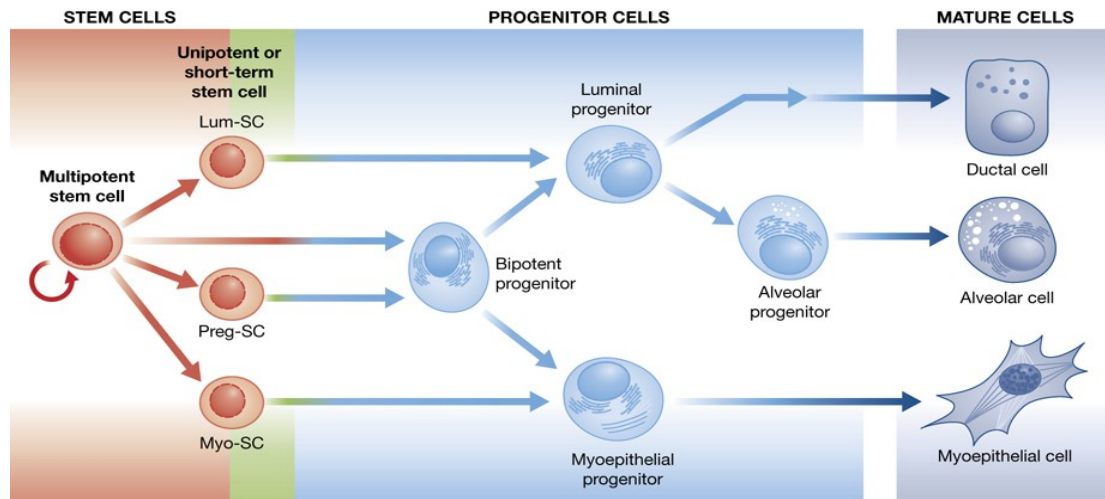


Figure 8: Model of the epithelial differentiation hierarchy in the mammary gland. A heterogeneous compartment of stem cells is present in mammary gland, in which the multipotent stem cell has greater self-renewal capacity than the unipotent stem cells (Myo-SC: myoepithelial-stem cell, Lum-SC: luminal-stem cell, Preg-SC: short term pregnancy-stem cell). The bipotent progenitors develop into either luminal or myoepithelial progenitor. Myoepithelial cells and luminal cells are formed as the ducts grow out postnatally during puberty. On initiation of pregnancy, myoepithelial and luminal cells are generated to synthesize and secrete milk (Visvader and Lindeman, 2011). Reproduced with permission.

1.2.3 Development and hormonal control of the mammary gland

At puberty and pregnancy stages, the mammary gland undergoes tissue remodeling in response to hormonal stimuli (Richert *et al.*, 2000, Hovey *et al.*, 2002). During puberty, estrogen and growth hormone function together to initiate mammary duct elongation. During pregnancy, other hormones such as progesterone (Pg) and prolactin (PRL) work coordinately to stimulate alveolar formation for production of milk for the young. Morphologic changes to the mammary gland are influenced by the presence and secretion level of hormones through paracrine actions and by transcription factors that modulate mammary stem cells activity (Asselin-Labat *et al.*, 2006, Joshi *et al.*, 2010). During the post-pregnancy stage, mammary epithelial cells express estrogen and progesterone receptors to enable ductal elongation, branching and alveolar expansion through regulating cell proliferation and turnover of cells in estrous cycles. Both estrogen and progesterone also function in other organs such as the uterus, ovaries and the hypothalamus for regulation of sexual development (Hennighausen and Robinson, 2001).

Mammary gland development is controlled by a variety of steroid hormones and their receptors. Estrogen binds to two distinct estrogen receptors, ER α and ER β , which functions as transcription factors when binding of steroid hormone. ER α plays a role during normal ductal outgrowth and elongation during puberty (Bocchinfuso *et al.*, 2000). On the contrary, ER β deletion does not have significant effects on the development of alveolar or duct (Forster *et al.*, 2002). Progesterone and its cognate receptors (A and B isoforms) play a crucial function during pregnancy stage by inducing mammary ductal side branching essential for lobuloalveolar development (Briskin *et al.*, 1998, Atwood *et al.*, 2000). Progesterone receptor B (PR-B) primarily mediates progesterone proliferative effects during pregnancy (Bromberg and Darnell, 2000). Prolactin (PRL) is a protein hormone produced by the pituitary gland that stimulates mammary gland development and milk production (Bole-Feysot *et al.*, 1998). PRL has a direct function on the formation of alveolar bud, however it does not have any contributions in ductal side branching in adult mammary glands (Ormandy *et al.*, 1997). Prolactin (PRL), cooperate with cortisol and insulin to stimulate transcription of the genes that encode milk proteins (Ormandy *et al.*, 2003).

1.2.4 Risk factors and etiology of mammary carcinoma

The incidence rate of breast cancer is determined by sexual reproduction, lifestyle, age, and many other factors (Key *et al.*, 2001). The breast cancer risk is greater amongst women with early age at menarche, delayed age at first full term pregnancy, breast feeding duration and late age at menopause, all of which are associated with prolonged exposure to estrogen (Lester, 2010). Collaborative Group on Hormonal Factors in Breast Cancer (Beral and Collaborative Group on Hormonal Factors in Breast, 1997) reported that the use of oral contraceptives and postmenopausal hormonal replacement therapy increase the risk of this disease as these exogenous estrogen agents increase cancer cells proliferation and induce mutagenesis (Persson, 2000). More than 60% of all breast cancers are dependent on hormones such as estrogen for their growth (Pasqualini, 2004). One of the definite risk factors of breast

cancer is history of atypical hyperplasia, which has a higher prevalence of transforming to malignant tumor than non-atypical proliferative breast lesions. Women with high density breast tissue, that has higher density of epithelial component compared to fatty and connective tissue component, are more likely to develop breast cancer than women with low density breast tissue (McCormack and dos Santos Silva, 2006). Other risk factors correlated to higher risk of breast cancer include increase height (Green *et al.*, 2011), higher body mass index (Reeves *et al.*, 2007), obesity, alcohol consumption and exposure to irradiation (Lester, 2010).

The incidence of breast cancer is also significantly increased in women with family history of breast cancer such as women with one first-degree relative with breast cancer have higher risk as compared with those without family history of the disease (Pharoah *et al.*, 1997). Furthermore, hereditary breast cancer accounts for close to 15% of cases and is caused by germline mutations in cancer susceptibility genes such as *BRCA1*, *BRCA2* and *TP53* (Thull and Vogel, 2004, Monnerat *et al.*, 2007). BRAC1 and BRCA2 proteins are important in maintaining genomic stability for homologous recombination and DNA repair of normal cells (Gudmundsdottir and Ashworth, 2006). Genetic mutation in *BRCA1* and *BRCA2* are associated with familial breast cancers. Individuals inherit these gene mutations have a range of 50% - 87% lifetime risk of development of breast cancer. Loss of function of such as tumor suppressor genes can result in high grade tumor and breast cancer progression (Osborne *et al.*, 2004). The p53 tumor suppressor protein regulates genes involved in cellular processes including apoptosis, cell cycle, and senescence (Brosh and Rotter, 2009). It has been reported that over-expression of mutated p53 protein in breast cancer patient is associated with poor prognosis and a greater incidence of recurrence (Macdonald, 2004). Additionally, over-expression of HER2/neu, a transmembrane tyrosine kinase member of the epidermal growth factor receptor family, was observed in 30% patients with breast cancer. Several studies have concluded that over-expression of this receptor is associated with a poor survival outcome of breast cancer patients (Ross and Fletcher, 1998, Nunes and Harris, 2002).

Nevertheless, the beneficial factors such as healthy lifestyle, physical exercise, lower age of first pregnancy, having more children and prolonged breastfeeding is positively associated with a reduced risk of developing breast cancer (Baselga and Norton, 2002).

1.2.5 Development of mammary carcinoma

Breast cancer is a complex and heterogeneous disease that is developed during the process of lesions from epithelial hyperplasia to invasive carcinoma and eventually metastasis (Allred *et al.*, 2001, Polyak, 2007). Breast cancer is initiated from a series of transformation events (genetic or epigenetic) in a single cell. The subsequent tumor progression is the resultant of accumulation of various genetic alterations such as amplification of oncogenes and/or mutation/loss of tumor suppressor genes (Beckmann *et al.*, 1997). A study by Allred *et al.* (2001) has demonstrated that the development of breast cancer is a multistage progression involving series of intermediate hyperplastic lesions such as epithelial hyperplasia, atypical ductal hyperplasia (ADH), followed by growth into non-invasive *in situ* carcinoma (ductal carcinoma *in situ* or lobular carcinoma *in situ*), invasive carcinoma, and finally metastatic cancer (Allred *et al.*, 2001). Normal breast duct consists of an epithelial cells layer and a myoepithelial cells layer that are separated from the stroma by a basement membrane. The ducts are surrounded by an interstitium consists of extracellular matrix (ECM) and stromal cells (e.g., endothelial cells, fibroblasts and leukocytes) (Man and Sang, 2004, Man, 2007). ADH is a premalignant lesion characterized by the presence of abnormal cell layers within the duct or lobule. The epithelial cells in ADH are abnormal in number, size, shape, appearance, and even excessive growth of cells in the ducts or lobules. ADH triggered by perturbed hormonal levels, inflammatory response and neoplasia. ADH increases the lifetime risk for developing of breast cancer (Vargo-Gogola and Rosen, 2007). *In situ* carcinomas are composed of lobular carcinoma *in situ* (LCIS) and ductal carcinoma *in situ* (DCIS). DCIS is a non-invasive cancer in which abnormal outgrowth of cells are confined to the lumen of the mammary duct. LCIS is an abnormal outgrowth of cancer cells in the milk-

producing lobules. The presence of DCIS can greatly increase the risk of developing into invasive breast cancer (Khamis *et al.*, 2012) as it is a precursor lesion of invasive growth called invasive breast cancer (IBC) (Figure 9). Unlike DCIS, LCIS is not a precursor lesion for breast cancer (Rieger-Christ *et al.*, 2001). The risk of developing invasive and/or malignant breast cancer increases with each stage. There are mainly two types of IBC, the invasive ductal carcinoma (IDC) and the invasive lobular carcinoma (ILC). IDC is the most common invasive mammary carcinoma (70% of cases) as compared to ILC, which represents about 10% of all breast cancer cases. Advanced mammary carcinoma is associated with degradation of basement membrane and disruption of the mammary myoepithelial cells. Tumor cells invade neighboring tissues, spread to distant organs, and subsequently metastases may be occurred via bloodstream or lymph nodes and subsequently led to dissemination of tumor cells to distant organs such as the bone, lung, liver, and less frequently the central nervous system (Solomayer *et al.*, 2000, Mack *et al.*, 2004).

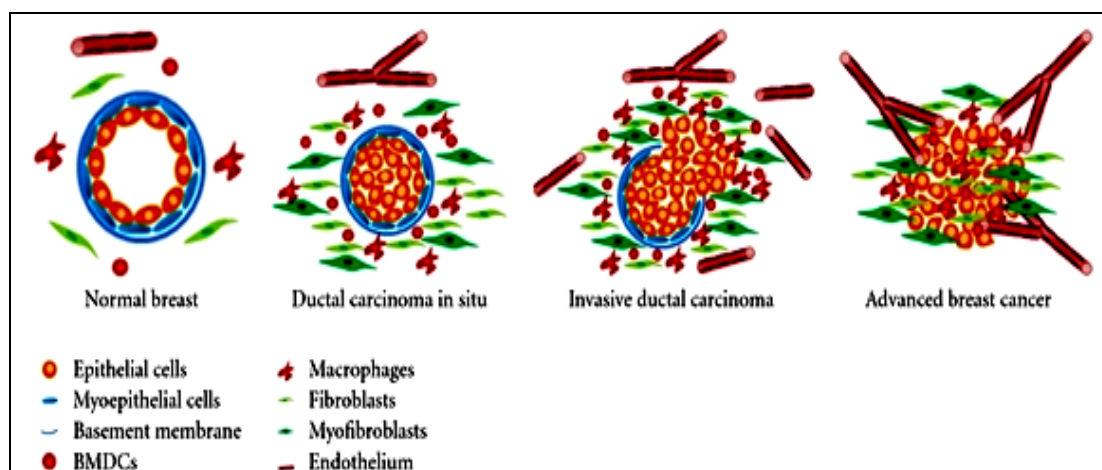


Figure 9: Breast cancer progression. Normal breast duct is composed of a layer of epithelial cells and a layer of myoepithelial cells. Ductal carcinoma *in situ* (DCIS) is an abnormal outgrowth of carcinoma cells confined within the ducts and lobules of the breast. When the myoepithelial cell layer and basement membrane are completely lost, carcinoma cells escape from the barrier of ducts or lobules, invade the surrounding breast tissues, and becomes invasive mammary carcinoma (Khamis *et al.*, 2012).

1.2.6 Microenvironment of mammary carcinoma

The microenvironment of mammary carcinoma plays an essential role in the control of neoplastic progression through dynamic reciprocity between cancer cells and their surrounding environment or tissues (Polyak and Kalluri, 2010). The mammary duct consists of epithelial cells surrounded by stroma components includes fibroblasts, myofibroblasts, endothelial cells, adipocytes, and various immune cells (Erler and Weaver, 2009). A thin layer of ECM lies between the epithelial cells and the stroma (Woodward *et al.*, 1998). The ECM is a rich in matrix metalloproteinases (MMPs) and growth factors that participate in neoplastic dissemination (Finger and Giaccia, 2010). There are four different types of cellular connections essential in the maintenance of the epithelial layer, which include desmosomes, adherens junctions, gap junctions, and tight junctions (Ehmann *et al.*, 1998). The functions of these structures are to restrict both cell movement and unlimited proliferation. Gap junctions act as a channel to mediate cell-to-cell communication and channeling cellular biological signals such as cytokines or products of tumor suppressor genes to the neighboring cells. Under normal physiological conditions, proper tissue architecture is preserved and/or retained by basement membrane and intercellular communication (Joyce and Pollard, 2009).

The normal tissue microenvironment acts as a barrier to tumorigenesis and exerts protective constraint against malignant transformation (Figure 10). The microenvironment can act as a permissive forces to tumor growth in the process of mammary carcinoma progression (Bissell and Hines, 2011). During invasion, tumor cells induce disruption of cell-cell contacts and cell-ECM interactions mediated by cell adhesion molecules such as integrins and cadherins. The basement membrane undergoes degradation and structural changes that lead to the destruction of normal tissue boundaries and provide a path for invasion of cancer cells (Khamis *et al.*, 2012). Therefore, the metastasis of mammary carcinoma is promoted by proteolytic degradation of neighboring tissue while motility of cancer cells is enhanced by the actions of chemokines, growth factors and also recruitment of stromal cells. (Friedl and Wolf, 2003). Several studies have demonstrated that cancer-associated fibroblasts stimulated

motility and proliferation of cancerous epithelial cells when they had direct cell interaction in co-culture (Korohoda and Madeja, 1997, Olumi *et al.*, 1998, Kalluri and Zeisberg, 2006). Endothelial cells are also recruited to the tumor microenvironment for ectopic blood vessels formation for metastasis (Folkman, 1992). The cellular transformation is regulated by interaction between epithelial cells, activated stromal cells as well as the ECM components (Khamis *et al.*, 2012). These cellular components in tumor microenvironment may function either as suppressive or promotional forces in the progression of mammary carcinoma (Bissell and Hines, 2011).

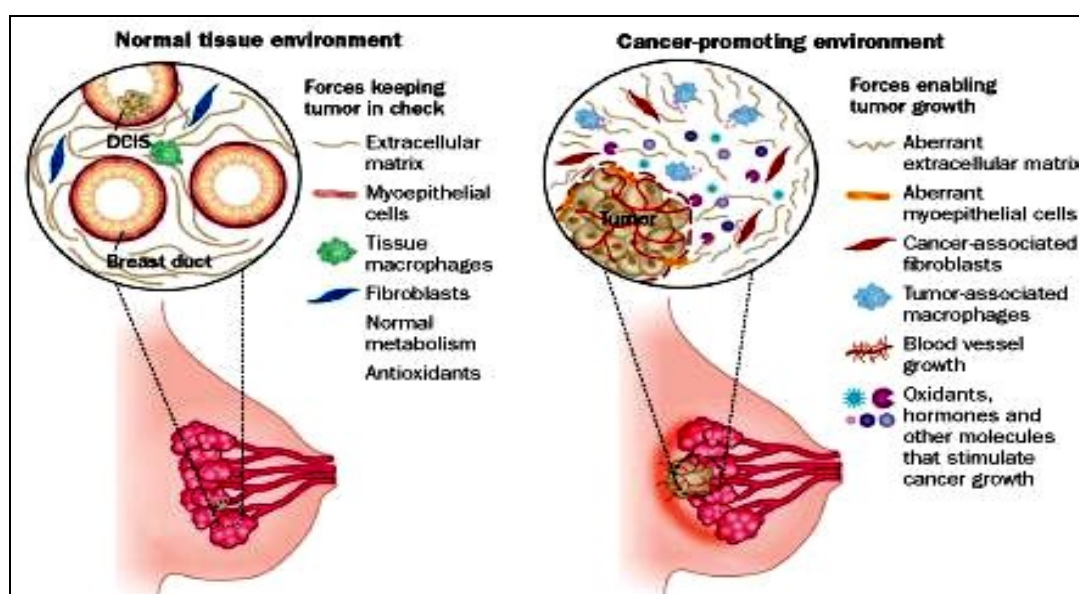


Figure 10: Microenvironment of breast cancer development. In a healthy breast (left), the normal tissue microenvironment acts as a barrier to tumorigenesis and exerts suppressive forces to restrain the dormant tumors under normal tissue homeostasis. In invasive cancer (right), the microenvironment can turn to be permissive conditions for tumor growth, and the combination of mutagens, inflammation, growth factors and other tissue-associated promotional forces can breach the barrier to tumor formation, resulting in aggressive growth of cancer (Bissell and Hines, 2011). Reproduced with permission.

1.2.7 Oncogenes in pathogenesis of mammary carcinoma

Pathogenesis of mammary carcinoma is associated with the accumulation of alterations of the genome. Genetic alterations that repress tumor suppressor genes and activate oncogenes may prime the affected cancer cells to be more susceptible to gain additional genetic damage that eventually led to instability in the tumor genome (Al-Kuraya *et al.*, 2004). Increased genetic alterations have been associated with clinicopathological features such as poorly differentiated pathology, metastasis and decreased survival (Al-Kuraya *et al.*, 2004, Ellsworth *et al.*, 2008a). Several oncogenes have been linked to mammary carcinoma progression including *ER*, *PR*, *HER-2/neu (ErbB-2)*, and *c-myc*. These genes are the major drivers of cancer progression and therefore become targets for therapeutic intervention.

(i) Estrogen receptor

The ER is one member of the nuclear hormone family of intracellular receptors and is activated upon binding of its hormone ligand, 17 β -estradiol (Dahlman-Wright *et al.*, 2006). ER functions as a DNA-binding transcription factor that regulates gene expression (Levin 2005). There are two main isoforms of ER namely ER α and ER β that encoded by *ESR1* and *ESR2* genes, respectively. In response to the stimulation of estrogen, ERs dimerize to form functionally active homodimer or heterodimer which then activate the transcription of the reporter genes containing estrogen response elements (Cowley *et al.*, 1997, Pace *et al.*, 1997). ERs are overexpressed in about 70% of breast cancer cases (ER-positive breast cancer). Upon binding of estrogen, ER induces mammary cells proliferation that subsequently lead to a marked increase in cell division and mutation rate (Burns and Korach, 2012). Furthermore, the process of metabolizing estrogen may produce genotoxic byproducts, which can directly damage DNA and subsequently resulted in point mutations (Burns and Korach, 2012). ER α expression is associated with more differentiated tumors while the significance of ER β expression in tumor remains controversial (Herynk and Fuqua 2004). One study suggested that ER β is correlated with cell proliferation and poor prognosis (Rosa *et al.*, 2008).

(ii) Progesterone receptor

The progesterone receptor (PR) is a transcription factor and a member of a group of intracellular steroid hormone receptors, which regulate gene expression at specific sites in DNA (Lange and Yee, 2008). There are two PR isoforms, PR-A (94 kDa) and PR-B (116 kDa), produced by the same gene located on chromosome 11 (Law *et al.*, 1987) that regulate different but overlapping target genes (Graham *et al.*, 2005). Comparing with PR-A, PR-B is a more potent transcriptional activator. PR-B has an effect on cellular proliferation and also differentiation of mammary epithelium. The biological function of ovarian and uterine are dependent primarily on PR-A (Mulac-Jericevic *et al.*, 2003). PR is expressed in reproductive tissue and has crucial roles in folliculogenesis, ovulation, implantation and pregnancy (Gadkar-Sable *et al.*, 2005). Recent clinical studies have shown that progesterone possess proliferative property in the normal human breast that is independent of estrogen, and is also one of the risk factor for mammary carcinoma (Anderson, 2002, Lee *et al.*, 2006). Furthermore, progesterone/PR acts in conjunction with mitogenic protein kinases and cell-cycle mediators to stimulate regulation of PR target genes (Lange and Yee, 2008).

(iii) HER2/neu

The HER2/neu (ErbB-2 or ERBB2) is a member of the epidermal growth factor receptor (EGF-R) family with tyrosine kinase activity and *HER2/neu* gene is found on chromosome 17q12 (Coussens *et al.*, 1985). HER2 is a membrane receptor tyrosine kinase implicated in the signal transduction pathways connected to cell growth and differentiation (Slamon *et al.*, 1989). Presumably, HER2 is an orphan receptor, which do not have a known ligand and is thus not activated by EGF family ligands (Olayioye, 2001). However, HER2 serve as a preferential dimerization partner for other members of the ErbB family (Olayioye, 2001). An estimated of 30% of breast and ovarian cancers contained *HER-2/neu* gene amplification and/or over-expression of its protein (Zhou and Hung, 2003). Over-expression of HER2/neu receptor in breast cancer has been reported to be associated with increased disease recurrence as well as worse prognosis (Ellsworth *et al.*, 2008b). This poor prognosis

may be due to genomic instability where breast cancer cells with higher frequencies of chromosomal modification is associated with enhanced cell proliferation and a more aggressive phenotype (Ellsworth *et al.*, 2008b). Additionally, genetic changes of the proto-oncogene *ErbB-2* (*HER2/neu*) are connected with elevated invasive phenotype and poor prognosis in breast cancer patients (Wilson *et al.*, 2002).

(iv) c-myc

The c-myc protein is a transcription factor and contains basic helix-loop-helix (bHLH) domain (Vennstrom *et al.*, 1982). The *c-myc* oncogene is over-expressed in about 15 - 25% of breast tumors (Deming *et al.*, 2000) and is implicated in breast cancer cell growth, transformation, angiogenesis, as well as cell cycle control (Chen and Olopade, 2008). Numerous studies have consistently observed the positive correlation between amplification of *c-myc* gene with breast cancer progression and poor clinical outcome (Chen and Olopade, 2008). Therefore, *c-myc* gene amplification is identified as a strong prognostic marker in predicting early recurrence in patients with node-negative breast cancer (Schlotter *et al.*, 2003).

1.2.8 Histological and molecular grading systems in mammary carcinoma

Histological-based grading system provides a method to distinguish well-differentiated tumors from poorly differentiated tumors. Grade 1 refers to tumors that are well-differentiated and demonstrates good prognosis, whereas Grade 3 is poorly-differentiated tumor and it is more likely to spread (Elston and Ellis, 1991). Although histological based grading system is widely used in the past, it may not be clinically informative as majority of breast cancer cases are fall under Grade 2 (Sotiriou *et al.*, 2006). The American Joint Committee on Cancer (AJCC) staging system of breast cancer serves is a standard for grouping patients with respect to prognosis. Therapeutic options are chosen based on several factors such as tumor size, lymph node status, hormone receptor status, HER2/neu status, and menopausal status. The AJCC has designated the staging system by

TNM classification to define breast cancer, where T to tumor size, N to lymph node involvement and M to distant metastasis (Singletary *et al.*, 2002). TNM refers to the presence of invasive or non-invasive tumor, the tumor size, the presence of cancer cells in lymph node and the presence of secondary metastasis of the tumor cells. In addition to the clinical TNM staging, current therapeutic options are preferably combined with histopathological grading, tumor size, lymph node, hormone receptor, HER2/neu and proliferation (Ki67) status. Therefore, molecular subtyping with immunohistochemistry (IHC) and fluorescence *in situ* hybridization (FISH) have later been established (Perou *et al.*, 2000). This classification may provide additional information on patient survival outcome. There are four molecular subtypes including luminal-like (luminal A or luminal B), HER2 enriched/over-expression, basal-like (triple negative) and normal-like. According to this classification, ER-negative breast cancer comprises of two tumor subtypes: basal-like and HER2-positive. Recent studies have demonstrated that these molecular subtypes differ in their responses to treatment and survival outcomes (Blows *et al.*, 2010, Dawood *et al.*, 2011). Other studies have precisely classified these molecular subtypes of breast cancer with respect to their PR, ER, and HER2 status and categorized them as luminal B (ER+ or PR+, and HER2+), luminal A (ER+ or PR+ and HER2-), basal (ER-, PR-, and HER2-) and HER2 (ER-, PR-, and HER2+) (Brenton *et al.*, 2005, Carey *et al.*, 2006). The luminal subtypes are the most common breast cancer subtypes and present good prognosis. Conversely, HER2 and basal-like subtypes show poor prognosis (Brenton *et al.*, 2005). As compared to other subtypes, the basal-like and HER2 tumors contain the highest rate of mutation. 80% of basal-like tumors with TP53 gene mutation which have been linked to poor outcomes (Cancer Genome Atlas Network, 2012). Currently, all breast cancers patients are tested for the ER, PR, and HER2 proteins expression. ER and PR are assayed by IHC while HER2/neu is examined by FISH. The protein profiling of tumors may provide useful information to design a better therapeutic treatment and predict survival outcomes for breast cancer patients.

1.2.9 Breast cancer diagnosis and treatment

There are different types of treatments available for breast cancer patients. The clinical symptoms observed in breast cancer patients are largely dependent on whether the tumor is confined to the breast or has metastasized. Primary therapies of local breast cancer include surgery (breast-conserving or mastectomy) and radiation therapy. Patients may opt for surgical removal of primary local tumor from the breast (breast-conserving) or to remove part of the breast (mastectomy). These patients may also be subjected to subsequent radiotherapy, chemotherapy, or hormone therapy to eradicate remaining cancer cells residing in the breast (Majure, 2000). Chemotherapy is an alternative treatment options that utilizes drugs to inhibit cell division and eventually the growth of cancer cells. Endocrine therapy involves blocking of hormones in order to attenuate cancer cells from growing (Majure, 2000). Some of endocrine therapies include competitors for ER and inhibitors of estrogen to counteract the effect of estrogen in breast cancer (Normanno *et al.*, 2005). Patients with elevated levels of ER and/or PR (i.e., luminal subtype) are treated with endocrine therapy (Normanno *et al.*, 2005). Other anti-estrogen agents for breast cancer patients include synthetic selective estrogen modulators (SERMs), such as tamoxifen, which acts as ER antagonist in breast cancer tissue, and aromatase inhibitors which inhibit the action of the enzyme aromatase to convert androgens into estrogens (Osborne, 1999). Tamoxifen has an agonist or antagonist effect depending on the molecular profile of its target (Jordan *et al.*, 2001). It reduces the development of breast cancer in both pre- and post-menopausal women who are at risk for the disease (Schlotter *et al.*, 2003). ER status is utilized as an indicator to deduce the sensitivity of breast cancer cells to tamoxifen and aromatase inhibitors (Fabian and Kimler, 2005). Raloxifene, which has anti-estrogenic behavior, is being widely used as a preventive chemotherapy for women who maybe at higher risk of developing of breast cancer (Oseni *et al.*, 2008). Additionally, a new type of endocrine therapy with ER antagonist effect, known as Fulvestrant, has also been developed. Fulvestrant acted by both down-regulating and degradation the ER expression (Kansra *et al.*, 2005). It can also be used after an anti-estrogen

therapy (Tamoxifen[®]) (Raina, 2004, Nicholson *et al.*, 2007). Targeted therapy is another treatment that utilizes drugs to identify and target specific cancer cells without causing any harm to normal cells. There are two types of targeted therapies available for treatment of breast cancer, which include the use of monoclonal antibodies and tyrosine kinase inhibitors (Crown *et al.*, 2012). One example is the use of PARP inhibitors as targeted therapy against triple-negative breast cancer (Crown *et al.*, 2012). Moreover, HER2/neu is the primary target of humanized monoclonal antibody trastuzumab (Herceptin[®]), which target the extracellular domain of this receptor and blocks the effects of HER2 in conveying growth signals to breast cancer cells (Kurokawa *et al.*, 2000). Therefore, patients with HER2 amplified (HER2+) tumors are given trastuzumab as monotherapy. Alternatively, this targeted therapy can be supplied to patients in combination with standard chemotherapy (Slamon *et al.*, 2001). However, majority of patients with HER2+ metastatic breast cancer who responded to trastuzumab at initial treatment stage eventually developed resistance within a year of treatment and some patients even relapse despite trastuzumab-based therapy (Cobleigh *et al.*, 1999, Vogel *et al.*, 2002).

Although clinical trials for combinational therapies of anti-estrogen and anti-HER2/neu treatment showed promising results (Kurokawa *et al.*, 2000), it has been reported that HER2-positive breast cancers have lower sensitive to estrogen modulation due to HER2 and ER cross-talk (Kurokawa and Arteaga, 2003). Development of resistance to therapeutic drugs (*de novo* or intrinsic resistance) is still a major barrier to effective treatment of breast cancer. It has been reported that some patients did not respond to therapy due to intrinsic drug resistance and multiple signaling pathways regulating the oncogenesis of breast cancer. Cross-talk between the ER and several growth factor signaling pathways has been widely recognized (Schiff *et al.*, 2004). Even in the absence of estrogen, cancer cells can still use growth factor signaling pathways as a compensatory mechanism and acquire anti-estrogen drug resistance (Schiff *et al.*, 2004).

A new recombinant humanized monoclonal anti-HER2 antibody, Pertuzumab, is currently being investigated. Pertuzumab binds to extracellular dimerization domain of HER2 and inhibits the heterodimerization of HER2 with other HER receptors or EGF receptors, thereby preventing activation of HER2 signaling pathways (Metzger-Filho *et al.*, 2013). Formulation of small molecule tyrosine kinase inhibitor (TKI) may reduce the onset of resistance and can be used in combination with targeted therapies. Example of TKI includes Bevacizumab[®] which is an anti-angiogenic molecules targeting VEGF-A, and anti-insulin growth factor 1 (IGF-1) therapy (Johnston, 2006). Hence, a multi-targeted therapeutic approach may offer a promising treatment for breast cancer patients.

1.3 Trefoil factors

The human trefoil factors (TFFs) are a family of proteins comprising of three members, which comprise of TFF1 (pS2) that was firstly identified as an estrogen-responsive gene in MCF-7 human breast cancer cell line (Jakowlew *et al.*, 1984, Nunez *et al.*, 1987), TFF2 (Spasmolytic polypeptide, SP) (Tomasetto *et al.*, 1990, Beck *et al.*, 1996), and TFF3 (intestinal trefoil factor, ITF) (Suemori *et al.*, 1991, Schmitt *et al.*, 1996). TFF1 was the first member of the family identified via cDNA cloning of estrogen-responsive gene from a breast cancer cell line (Masiakowski *et al.*, 1982, Jakowlew *et al.*, 1984). TFF2 was almost coincidentally isolated in porcine pancreas (Jørgensen *et al.*, 1982, Thim *et al.*, 1985). Subsequently, TFF3 from rat intestine was the third human trefoil factor described (Suemori *et al.*, 1991). The trefoil proteins have also been identified in other mammals such as rat, mouse and chimpanzee (Thim and May, 2005). TFF peptides are specifically synthesized in mucin producing cells of gastrointestinal (GI) tract and thus are characteristic secretory products of the mucous epithelia. Physiologically, TFF1 and TFF2 are expressed in human stomach mucosa and TFF3 is predominantly expressed in GI tract and colon. Evidence indicated that TFF peptides are involved in maintaining the integrity of GI epithelium by supporting mucosal defense and repair mechanism (Taupin and Podolsky, 2003, Hoffmann,

2004). The gene encoding human TFF peptides are found on chromosome 21q22.3 in a 55 kb gene cluster region (Seib *et al.*, 1997) (Figure 11). TFF peptides have seven conserved cysteines residues, of which six are connected to each other by disulfide bonds in a specific order, forming a three-cyclic structure, whereby the whole peptide chain is folded and shaped like a "clover". This structural motif domain is named as trefoil domain or P-domain (Thim, 1989, Polshakov *et al.*, 1997). Trefoil domain is cysteine-rich module that forms the functional unit for TFF peptides (Wright *et al.*, 1997, Wright, 1998, Thim and May, 2005, Hoffmann, 2006) and confers proteolytic stability and resistance to acidic degradation (Suemori *et al.*, 1991). TFF peptides contain either one or two trefoil domains, which consist of 42 - 43 of highly conserved or semi-conserved amino acids (Thim, 1989, Poulsom *et al.*, 1997). TFF1 and TFF3 each contain one trefoil domain, whereas TFF2 contains two (Figure 11). Both TFF1 and TFF3 have a seventh cysteine residue at the carboxyl terminus of the peptides that facilitates homodimerization and intermolecular interactions with other proteins (Thim and May, 2005). TFF1 and TFF3 can exist in several different molecular forms such as monomers, homodimers and heterodimers. TFF dimers are predicted to be more biologically active than monomers. The monomer and homodimer of TFF1 are more asymmetric than that of TFF3 and such differences may account for the divergent biological activities and specificity (May *et al.*, 2003).

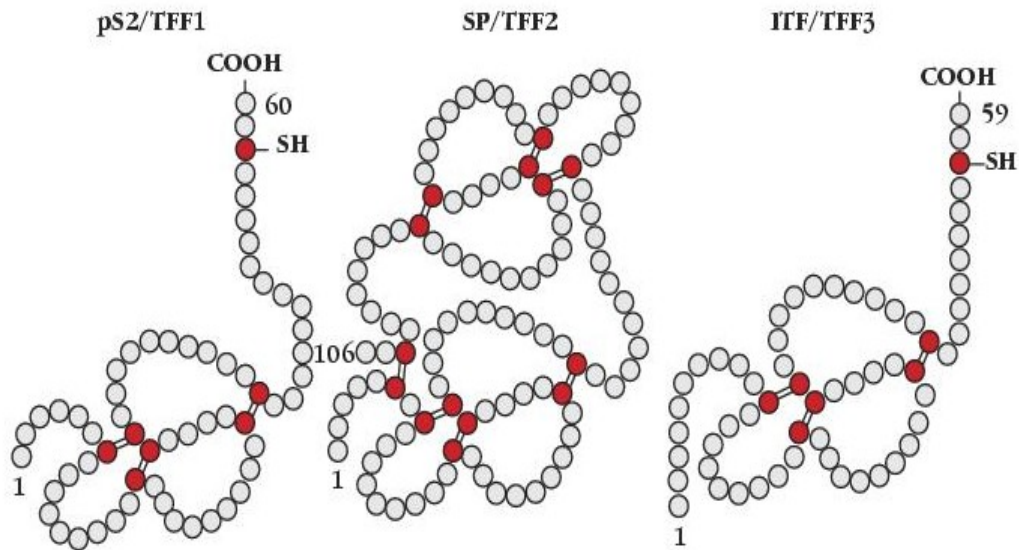


Figure 11: Human TFF peptides. Conserved cysteines residues (red circle) connected with each through disulfide bonds in a specific order to form a three-cyclic structure (Thim and May, 2005). Reproduced with permission.

1.3.1 Gene structure and regulation of TFF

All three human TFF genes are located in clusters on chromosome 21q22.3 in a sequential arrangement within a single 55 kb genomic region in the order telomere-TFF1-TFF2-TFF3-centromere (Hattori *et al.*, 2000) (Figure 12). TFF1 and TFF3 genes contain three exons, while TFF2 contains four exons. These exons encode the amino terminal signal peptide, followed by the trefoil domain, and the carboxyl terminal acidic motif, respectively. Transcription of these three genes is directed towards the centromere. In mouse genome, a 40 kb region located on chromosome 17q is found to resemble the human TFF gene (Ribieras *et al.*, 2001). Conservation of TFF gene cluster between different organisms (mouse and human) implied that TFF expression is partially regulated by a locus activation region (Thim and May, 2005). The promoter region consists of an estradiol responsive element (ERE) (Berry *et al.*, 1989), and also contains a complex enhancer region responsive to the proto-oncoproteins c-Ha-ras, tumor promoter TPA, epidermal growth factor (EGF) and c-jun (Nunez *et al.*, 1989). Several transcriptional factors, regulatory proteins and epigenetic factors including estrogens, progesterone, epidermal growth factor, basic fibroblast growth factor, upstream stimulating

factor (USF), hepatocytes nuclear factor, GATA-6 and Ha-Ras/AP-1 coordinately regulate the cell-type specific expression of TFF genes (Beck *et al.*, 1999, Al-azzeah *et al.*, 2002, Borthwick *et al.*, 2003).

TFF1 promoter region contains an ERE that lies between 332 to 428 bp upstream of the transcriptional start site. Activation of TFF1 expression is induced by estrogen in ER+ mammary carcinoma cells, acting in a synergistic manner with the steroid receptor coactivator-1 (Src-1), via the AP-1 and ERE at the TFF1 promoter (Barkhem *et al.*, 2002a, Barkhem *et al.*, 2002b). Estradiol-mediated regulation of TFF1 gene expression has been observed in mammary carcinoma (Rio *et al.*, 1987), but has not been conclusively demonstrated in other tissues. The presence of other regulatory elements may contribute to the expression of TFF1. An example is GATA-6, which is an endodermal transcription factor expressed in various tissues including pancreas gut, liver, pancreas, and lung. GATA-6 activates expression of TFF1 and TFF2 but not TFF3 (Al-azzeah *et al.*, 2000). Moreover, TFF1 gene is down-regulated by NF- κ B and C/EBP β (Dossinger *et al.*, 2002). In addition to the genetic regulation of TFF1 expression, epigenetic mechanisms also modulate TFF1 expression levels. The proximal promoter/enhancer region of TFF1 gene contains several CpG islands. The TFF1 gene is subject to tissue-specific methylation of its proximal enhancer region and the extent of methylation correlates with its expression (Martin *et al.*, 1997, Fujimoto *et al.*, 2000, Carvalho *et al.*, 2002).

TFF2 was identified as a side product from the purification of insulin from porcine pancreas (Sands and Podolsky, 1996). There is limited knowledge or literature on the transcriptional regulatory elements of this gene but the transcription factors such as GATA-6, STAT-6, upstream stimulating factors (USF) and Peroxisome proliferator-activated receptor gamma (PPAR γ) activate TFF2 gene expression (Al-azzeah *et al.*, 2000, Baus-Loncar *et al.*, 2004). In contrast, NF- κ B and C/EBP β down-regulate TFF2 expression (Dossinger *et al.*, 2002).

TFF3 promoter region contains two ERE (Baus-Loncar *et al.*, 2004). Induction of TFF3 expression has been shown to be estrogen-dependent in breast cancer cells (May and Westley, 1997a). The pro-inflammatory cytokine IL-6 induces TFF3 gene expression via STAT3 transcription factor (Tebbutt *et al.*, 2002). TFF3 promoter contains HIF-1 response elements that results in increased TFF3 expression mediated by HIF-1 under hypoxia (Furuta *et al.*, 2001). As demonstrated in TFF1 and TFF2, NF- κ B and C/EBP β down-regulate the expression of TFF3 gene via four NF- κ B and two C/EBP β binding motifs (Dossinger *et al.*, 2002, Loncar *et al.*, 2003).

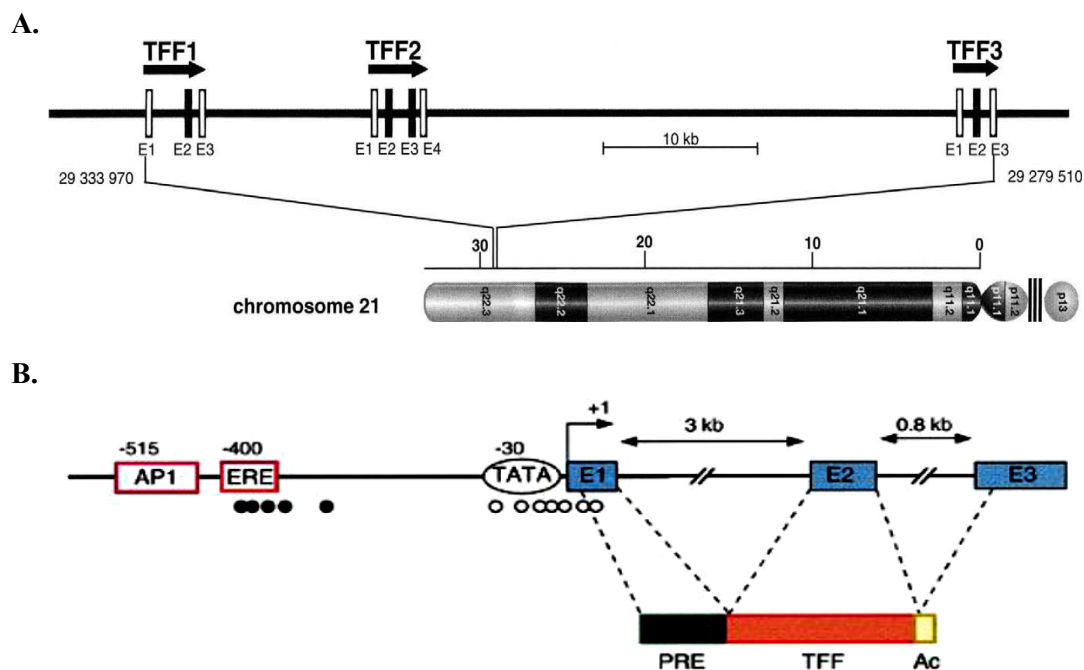


Figure 12: Chromosomal localization of human TFF genes. A, TFF cluster on chromosome 21q22.3. The exons (e.g., E2 or E3) encode human trefoil domains and the first exon (E1) encodes the signal sequences of the precursors of TFF proteins. B, Regulatory elements such as ERE at the promoter region of trefoil factors (Ribieras *et al.*, 1998). Reproduced with permission.

1.3.2 TFF protein

Mammalian orthologous sequence analysis of TFF across different species, including human, rat, mouse, canine, pig, and chimpanzee, shows an overall amino acid sequence conservation of 52% with a 57% homology in the trefoil domain (Thim and May, 2005). The amino acid sequence of the trefoil domain in TFF3 is conserved among mammalian species with an orthology of 67% (Thim and May, 2005). TFF3 shares the relatively low level of amino acid sequence homology of 36% compared to TFF1. However, TFF3 contains many of similar elements that are common to members of TFF family (Sands and Podolsky, 1996). TFF peptides are synthesized with a signal sequence for secretion of 21 or 27 amino acid residues that are proteolytically spliced away when passing through the endoplasmic reticulum. The secreted mature form of TFF peptides comprises a signal peptide, one or two trefoil domain (s), and a carboxy-terminal acidic domain. Despite having similar isoelectric points, TFF1 and TFF3 differs significantly in their hydrodynamic properties, distribution of surface amino acids and overall charge (Emami *et al.*, 2004).

TFF1 possesses 60 amino acid residues, encoding a 9 kDa protein and a single trefoil domain consists of 42 amino acid residues. TFF2 contains 106 amino acid residues, encoding a 14 kDa protein, and two trefoil domains consisting 43 residues and 42 residues respectively in the first and second trefoil domains. The first trefoil domain in TFF2 differs as it contains an additional amino acid residue. TFF3 consists of 59 amino acid residues, encoding a 7 kDa protein, and contains a single trefoil domain of 42 amino acid residues (Figure 13). In addition to the six conserved cysteine residues in the trefoil motif, TFF1 and TFF3 contain a seventh cysteine residue located three amino acids away from the carboxyl terminus of the protein. This allows homodimerization, via a disulfide bond with the seventh cysteine residue of the other trefoil factors as well as heterodimerization, via intramolecular disulfide bonds with other proteins (May *et al.*, 2003, Thim and May, 2005, Westley *et al.*, 2005). TFF2 has two trefoil domain cysteine residues that can produce an intermolecular disulfide bond (Thim, 1989).

The biological potencies and activities of TFF peptides are dependent on structural differences or interaction with other proteins. Homodimerization is critical for the biological functions of TFF, particularly its ability to stimulate cell migration and proliferation *in vitro* (Marchbank *et al.*, 1998, Calnan *et al.*, 1999, Prest *et al.*, 2002) as well as protection of the gastric against damage *in vivo*. An *in vitro* wound healing model, TFF1 dimer significantly increased cell migration of human colorectal cell line as compared to TFF1 monomer (Marchbank *et al.*, 1998). Dimeric TFF1 significantly reduced gastric damage *in vivo*, while monomeric TFF1 was ineffective. Previous studies utilizing a cell line model of epithelial barrier function have shown that specific mucins interacted with specific trefoil factors to act in a coordinate manner for protection of mucosa (Kindon *et al.*, 1995). Heterodimerization of TFF1 with mucin MUC5AC through C-terminal disulfide interaction promotes mucosal protection in the normal GI tract where these two proteins are co-localized (Longman *et al.*, 2000, Ruchaud-Sparagano *et al.*, 2004). An animal model study suggested that glycosylation of TFF2 is more effective than its non-glycosylated form in the protection against gastric damage (Playford *et al.*, 1995). Homodimerization appears to be required for the protective functions of TFF3 in the GI tract (Carrasco *et al.*, 2004). TFF3 and mucin MUC2 have been shown to co-localize in the GI tract although no direct protein-protein interactions have been elucidated (Longman *et al.*, 2000). Formation of the heterodimer between trefoil factor interactions(z) 1(TFIZ1) and TFF1 is observed in the mucus secretory cells of the stomach. In gastric cancer, the co-expression of these two proteins is deregulated whereby the expression of TFF1 in the absence of TFIZ1 is correlated with both invasive and also metastatic phenotype (May *et al.*, 2009). Piezo1 is a novel TFF1 binding protein which is crucial for TFF1-mediated cell migration (Yang *et al.*, 2014).

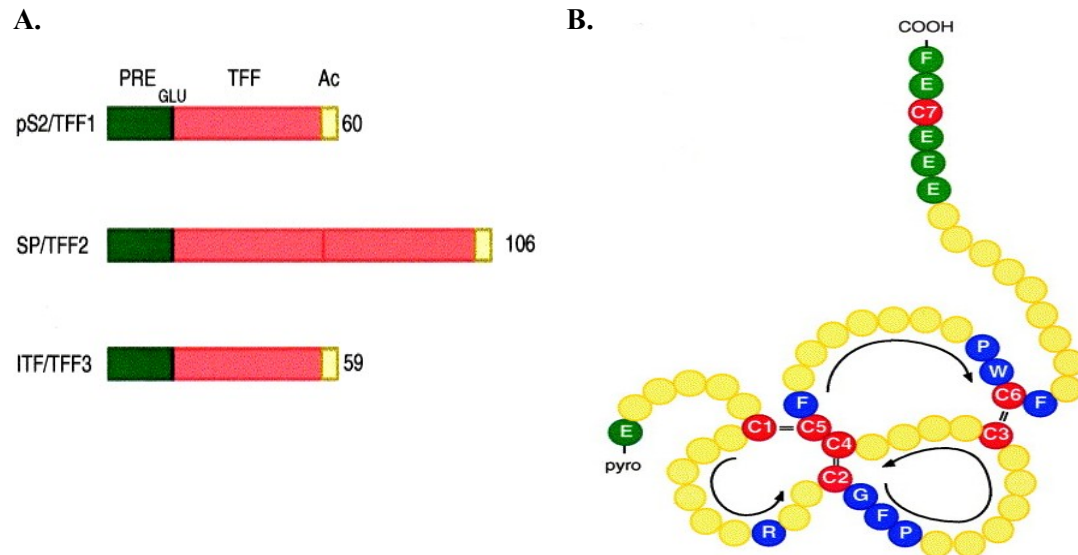


Figure 13: TFF protein. A, Conserved protein primary structure of the three human TFFs, including a signal peptide (PRE), one or two TFF domains (TFF) and a carboxy-terminal acidic domain (Ac). B, Trefoil secondary structure. The conserved cysteine residues in the trefoil domain formed disulfide bond in a C1-C5, C2-C4, and C3-C6 configuration to create three loops reminiscent of a cloverleaf. Conserved cysteine (C7) at the carboxy terminus facilitates homo- hetero-dimerization (Ribieras *et al.*, 1998). Reproduced with permission.

1.3.3 Normal expression patterns and localization of TFF proteins

TFF proteins have protective and restorative functions in normal tissue (GI tract) where they are normally expressed, but they exhibit adverse effect in cancerous tissues where they are pathologically expressed. Normal distribution of these proteins is primarily in the GI tract although they have specific localization within the tract to perform their functions in gastric mucosa.

TFF proteins are usually localized to the gastric mucosa with TFF1 and TFF2 normally expressed in the gastric epithelia. TFF proteins are not only expressed in GI tissues, but are also expressed in other tissues such as bronchial and urogenitary tracts (May and Westley, 1997b, Oertel *et al.*, 2001). TFF1 and TFF3 are expressed in human hypothalamus, gastric juice and urine, suggesting autocrine, paracrine and endocrine functions for these proteins (Rio *et al.*, 1987, Hoffmann and Jagla, 2002). TFF proteins are major components found in the GI mucosa, but each is expressed differentially. TFF1 and TFF2 expression are

found in the gastric epithelial, while TFF3 in the goblet cells of intestine. Both TFF1 and TFF2 are expressed in the stomach but have different expression patterns within this organ. TFF1 is mainly expressed in the superficial cells of the GI tissue (Ruchaud-Sparagano *et al.*, 2004), whereas basal cells of the gastric tissue express TFF2 (Minegishi *et al.*, 2007). TFF1 expression is not observed in the uterus, spleen, muscle, small intestine, lung, kidney, brain, hepatocellular, testis, pancreas, colon, cardiac, and skin (Bonkhoff *et al.*, 1995, Ribieras *et al.*, 1998). Low levels of TFF1 expression are seen in the mammary gland and breast epithelium (Piggott *et al.*, 1991, Hanby *et al.*, 1993). TFF2 is expressed in the Brunner's glands of the duodenum (Ribieras *et al.*, 1998) and TFF3 is predominantly expressed in the small and large intestine, particularly the colon and duodenum (Taupin and Podolsky, 2003). TFF3 has also been shown to be expressed in the lung, salivary glands, the cornea, conjunctiva tissue, brain, and lymphoid tissue (Cook *et al.*, 1999, Jagla *et al.*, 1999, Göke *et al.*, 2001, Emami *et al.*, 2004) where they are postulated to possess function in inflammation and epithelial ulceration.

1.3.4 Expression of TFF3 in human mammary carcinoma

Elevated expression of TFF proteins has been reported in a number of human cancers, including breast, prostate, esophagus, stomach, liver, pancreas and intestines (Emami *et al.*, 2004). Therefore, TFF proteins may have a pivotal function in the development and progression of human cancer.

In the human breast, TFF3 protein is normally present in breast epithelial cells at the lobules and ducts. The function of TFF3 in the human breast may be to protect and maintain the integrity of the epithelial surface (May and Westley, 1997a, Poulsom *et al.*, 1997). Co-expression of TFF1 and TFF3 was observed in breast epithelial cells. Poulsom *et al.* (1997) analyzed the expression of TFF3 in breast cancer tissue by *in situ* hybridization and observed that TFF3 was highly expressed in both non-invasive and invasive lobular and ductal breast cancer. A recent cohort study on breast cancer patients has shown that increased TFF3 expression in 89% of *in situ* mammary carcinoma and in 83% of invasive mammary

carcinoma (Ahmed *et al.*, 2012). In breast cancer cells, TFF3 protein expression was observed to be strongly associated with the expression of estrogen and progesterone receptors. Additionally, it has been shown that the expression of TFF3 is regulated by estrogen (May and Westley, 1997a).

1.3.5 TFF3 signaling

Although TFF3 plays a critical part in tumor progression, the signaling pathways of TFF3 are not fully understood. A receptor for TFF3 protein has not yet been identified to elucidate the mechanism of TFF3 in both normal and pathological contexts. Numerous studies have shown that TFF proteins may indirectly bind to other proteins or secreted factors that may activate signaling cascades for promoting the biological effects of TFF3 protein. Using immunoprecipitation followed by cross-linking, Chinery and Cox (1995) observed that TFF3 binds to a phosphorylated tyrosine-containing peptide of 28 kDa. Another study has demonstrated that TFF3 binds to 50 kDa membrane glycoprotein in the small intestine crypts and also in the mucous cells of the gastric glands (Tan *et al.*, 1997). A recent study speculated that Sp-1 binds to the core region of TFF3 promoter (positioned from -300 bp to -296 bp) resulting in increased TFF3 promoter activity and the subsequent stimulation of TFF3 expression (Sun *et al.*, 2014). Additionally, ERG is a ETS transcription factor and directly binds to ETS response elements in the TFF3 promoter in ERG-rearranged prostate cancer cell lines to induce invasive potential of castration-resistant prostate cancer (Rickman *et al.*, 2010). Signaling pathways that have been identified for potentiating the biological functions of the TFF3 protein include EGF, G-protein, and cyclooxygenase (COX).

(i) Epidermal Growth Factor (EGF)

Although TFF3 has not been reported to bind directly to a receptor, it is able to signal through specific pathways via indirect activation. Previous studies have proposed that TFF3 transmits signal indirectly through the activation of EGF-R (Liu *et al.*, 1997). EGF-R signaling pathway is important for tumor growth and over-expression of EGF-R is correlated

with metastasis potential, poor survival and higher relapse rates in human tumors (Radinsky *et al.*, 1995, Ozgul *et al.*, 1997). Upon stimulation by TFF3, EGF-R is activated and receptor tyrosine protein kinase activity is enhanced. Treatment of gastric cancer cell lines with TFF3 resulted in phosphorylation of the EGF-R, indicating that TFF3 has the ability to indirectly activate EGF receptor (Liu *et al.*, 1997, Kanai *et al.*, 1998, Taupin *et al.*, 1999, Kinoshita *et al.*, 2000b). In addition, the pro-invasive effects of TFF1 and TFF2 were abrogated by treatment with EGF-R tyrosine kinase inhibitor and/or with the use of a dominant negative form of the EGF-R (lacking intracellular domain), suggesting that this pathway is essential for the pro-invasive function of these proteins. However, the pro-invasive effect of TFF3 was not affected by EGF-R tyrosine kinase inhibitors under the same experimental conditions, indicating that TFF3 induced invasion of kidney and colon cancer cells independent of EGF-R (Rodrigues *et al.*, 2003a). This raises the possibility that TFF3 may exert its functions through both receptors and signaling pathways (Rodrigues *et al.*, 2003a). This observation is supported by Yong *et al.* (2013) have identified a TFF3 specific binding receptor in the intestinal epithelial cells. The authors believed that EGF-R is unlikely to be the TFF3 receptor (Yong *et al.*, 2013). Several studies have demonstrated that TFF3 may transmit extracellular signals and promote cell proliferation and migration through activation of EGF-R (Hoffmann, 2007, Li *et al.*, 2011). Furthermore, the pro-angiogenic functions of TFF1 appear to be regulated in an EGF-dependent manner as pharmacological inhibition of EGF-R tyrosine kinase activity resulted in decreased TFF1-induced angiogenesis (Rodrigues *et al.*, 2003b).

(ii) Heterotrimeric G-proteins

Another potential signaling cascade activated by the TFF peptides is the heterotrimeric G-protein pathway. There is no experimental data to show that TFF peptides directly bind to G-protein receptors. Several studies indicate that the G-protein signaling pathway is important for the mitogenic functions of TFF1 and TFF3 (Faivre *et al.*, 2001, Rodrigues *et al.*, 2001). The TFF3- and TFF1-induced invasion of kidney and colonic epithelial cells were abrogated by the pharmacological inhibition of critical elements of the G-

protein signaling machinery including Rho small GTPase and thromboxane A2 receptor (TXA2-R). In contrast, the constitutively activated forms of heterotrimeric G-proteins $G_{\alpha q}$ ($AG_{\alpha q}$), $G_{\alpha 12}$, $G_{\alpha 13}$ ($AG_{\alpha 12/13}$) and TXA2-R mimetic led to increased invasion of kidney and colonic epithelial cells promoted by these two proteins (Rodrigues *et al.*, 2001). Additionally, over-expression of TFF1 resulted in increased invasion mediated by Rho-independent and TXA2-R-dependent pathways (Rodrigues *et al.*, 2001) and ablation of $G\beta\gamma$ heterodimers resulted in decreased TFF-induced cellular invasion (Faivre *et al.*, 2001).

(iii) Cyclooxygenases COX-1 and COX-2

The pro-inflammatory molecules COX-1 and COX-2 have been identified as potential signaling mediators of the TFF peptides. Both molecules are proposed to contribute in the pro-invasive and pro-angiogenic functions of TFF peptides although experimental evidence is very limited. Expression of COX-2 has been postulated in tumor initiation and progression by regulating cell proliferation, migration, and invasion (Young *et al.*, 1992). Its oncogenic effect can be induced by several growth factors and oncogenes such as EGF-R tyrosine kinase, and pro-inflammatory cytokines (Vane *et al.*, 1998). It has been shown that inhibition of COX-1 and COX-2 led to the ablation of TFF1-induced invasion and angiogenesis (Rodrigues *et al.*, 2001, Rodrigues *et al.*, 2003a, Rodrigues *et al.*, 2003b). Therefore, TFF1 induces COX-2 expression to promote cellular invasion in human colonic cells (Emami *et al.*, 2001). TFF3 binds to intestinal mucosa and enhances production of nitric oxide via activation of cyclooxygenases (COX-2) pathway (Rodrigues *et al.*, 2001).

1.3.6 Biological functions of TFF3

TFF peptides have been implicated in stabilization of mucus and stimulation of normal epithelial restitution during mucosal repair. TFF peptides are rapidly expressed and secreted in an autocrine manner during GI injury. The secreted TFF peptides function as motogens to assist migration of epithelial cells into the wound, thereby providing a physical barrier in a process referred to restitution (Taupin and Podolsky, 2003) (Figure 14).

Additionally, TFF proteins are potent inhibitors that resist apoptosis and anoikis during the process of migration of the cell. Therefore, the biological functions of TFF proteins include (i) forming and stabilizing the mucus barrier, (ii) promoting rapid mucosal repair (restitution), (iii) modulating mucosal differentiation as well as (iv) modulating mucosal immune response (Hoffmann, 2004).

First lines of evidence suggesting that TFF proteins play a protective role arise from animal studies whereby rats were treated with the prostaglandin inhibitor indomethacin that causes ulceration of the GI tract. Combined prophylactic treatment of these animals with epidermal growth factor (EGF) and TFF3 led to remarkable reduction of gastric damage (Chinery and Playford, 1995, Playford *et al.*, 1995). Subsequently, this observation was confirmed by *in vivo* studies which showed administration of TFF2 and TFF3 proteins to confer protective and beneficial effects against chemical-induced damage of the gastric mucosal at a level comparable to prostaglandin-mediated cytoprotection (McKenzie *et al.*, 2000, Babyatsky *et al.*, 2009). Furthermore, knockout mice lacking TFF3 expression were more susceptible to dextran sodium sulfate-induced colitis and had a higher mortality rate than wild-type mice (Mashimo *et al.*, 1996). Mice with TFF1 and TFF3 deficiency exhibit impaired mucosal healing and eventually die due to high rate of apoptotic events of colon cells associated with severe colitis (Lefebvre *et al.*, 1996, Mashimo *et al.*, 1996). *In vitro* model systems also demonstrated that increased expression of TFF2 and TFF3 proteins significantly reduced colonic damage induced by multiple toxins insults on colon cancer cells and the protective effects of the TFF peptides were enhanced with co-expression of mucin glycoproteins (Kindon *et al.*, 1995). The function of TFF2 and TFF3 are mediated through the epithelial (E)-cadherin/catenin complexes, which is one of the common motogenic targets during cell migration (Liu *et al.*, 1997). TFF3 promoted cell migration by inhibition of E-cadherin function and tyrosine phosphorylation of β -catenin (Liu *et al.*, 1997, Efstathiou *et al.*, 1999). TFF3 also can stimulate down-regulation of E-cadherin, α - and β -catenin that inducing subsequent decrease in cell adhesion for enhancing cellular invasion and migration of cancer

cells (Liu *et al.*, 1997). The prophylactic effects of TFF proteins have been demonstrated in both animal and cell line models of GI tract injury. These data support that TFF proteins serve as beneficial factors in the maintenance of the epithelium of GI tract. Several mechanisms have been shown would be contributed to the protective and tumor suppressive roles of TFF proteins. For example, transgenic mice with over-expression of growth hormone (GH) exhibit elevated expression of TFF3 in the colon with enhanced survival, and mucosal repair during recovery from experimental colitis. These observations suggested possible interaction or cross-talk between EGF-R signaling with TFF3 expression in mucosal repair mechanism (Williams *et al.*, 2001). Furthermore, the motogenic function of TFF3 peptides in restitution of GI epithelium is probably through a TGF β -independent pathway (Dignass *et al.*, 1994, Sands and Podolsky, 1996).

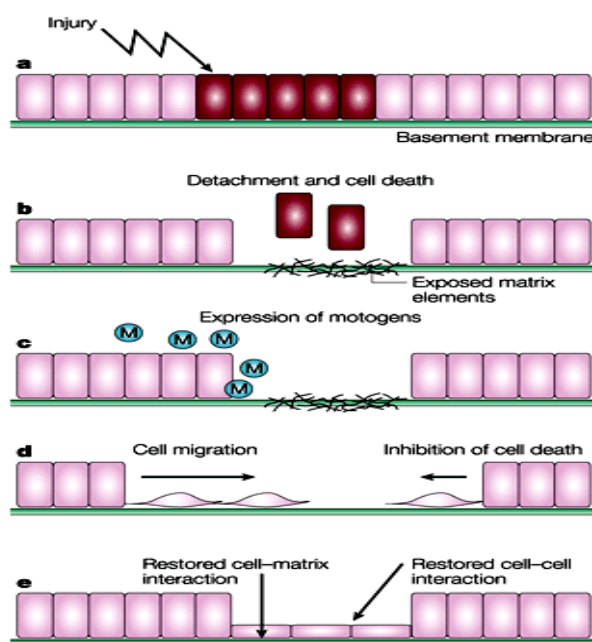


Figure 14: The different steps of mucosal restitution. a. Local mucosal damage. b, cellular detachment and apoptosis immediately occurred. c, activation of adjacent mucosal cells at the wounded areas to release motogenic agents (motogens; M) such as trefoil factors and to initiate the mechanism of restitution or repair. d, this process followed by migration of epithelial cells and inhibition of cell death. d, which is accompanied by mechanisms that prevent detachment-induced cell death. e, restoration of cell-matrix interaction and cell-cell interaction at the wounded areas (Taupin and Podolsky, 2003). Reproduced with permission.

1.3.7 Oncogenic potential of TFF3

TFF3 may serve as either tumor suppressor genes or potential tumor promoting factors depending on tissue localization. Although TFF3 protein play a protective and restorative role in the GI tract where it is normally localized, TFF3 protein is over-expressed in various tumor tissues including those of pancreatic, prostate, breast, liver, endometrium, ovary, uterus, esophagus, and bladder (May and Westley, 1997b, Emami *et al.*, 2004). Many reasons can account for this duality in function including the positive association between inflammation and increased TFF3 expression in the microenvironment of the tumor, epigenetic modification of TFF3 expression, or activation of oncogenes that increased the expression of TFF3. However, the mechanisms of TFF3-mediated activation of oncogenes in cancerous cells have yet to be elucidated. Increasing experimental studies demonstrated the tumor promoting actions of TFF peptides implicated in tumor growth and progression.

(i) Proliferation

There is very few evidence demonstrating the role of TFF peptide in regulating cell cycle progression. Autocrine production of TFF3 significantly enhanced proliferative capacity in mammary carcinoma cells (Xu *et al.*, 2005, Kannan *et al.*, 2010). Forced expression of TFF3 in mammary carcinoma cell lines markedly increased the total cell number as a result of enhanced cell proliferation and survival (Kannan *et al.*, 2010). However, over-expression of TFF3 suppressed growth of human colon cancer cells and was shown to function as an inhibitory factor for proliferation of colonic neoplasm (Uchino *et al.*, 2000). Furthermore, depleted expression of TFF3 using an antisense oligonucleotide significantly reduced proliferation of human gastric carcinoma cell line (Chan *et al.*, 2005a).

(ii) Apoptosis

Resisting apoptosis is one crucial characteristic during oncogenesis. Studies have shown that all the TFF family members play an anti-apoptotic role. TFF1 has been demonstrated to prevent gastric carcinoma cells from undergoing anoikis, chemical-induced apoptosis, as well as BCL-2-antagonist of cell death (BAD)-induced apoptosis (Bossenmeyer-

Pourie *et al.*, 2002). Forced expression of TFF3 in colon carcinoma cells prevented the cells against serum starvation-induced and drug-induced apoptosis, which is dependent on PI3K activity (Kinoshita *et al.*, 2000a, Taupin *et al.*, 2000a). Autocrine TFF3 stimulated survival of mammary carcinoma cells increased BCL-2 protein expression (Kannan *et al.*, 2010). A study reported that TFF3 activated Akt/protein kinase B survival pathway in the process of mucosal repair (Taupin *et al.*, 2000a). The p53-dependent apoptosis in gastric carcinoma cell lines following treatment with etoposide was markedly abrogated by forced expression of TFF3 (Taupin *et al.*, 2000a). Concordantly, antisense TFF3 significantly increased adriamycin-induced apoptosis in gastric carcinoma cells (Chan *et al.*, 2005a).

(iii) Anoikis

Anoikis is a form of anchorage-dependent cell death program induced by cell detachment. It is a relatively important event for oncogenic transformation as well as cancer progression. It has been observed that forced expression of TFF3 prevented anoikis in intestinal epithelial cells, which is mediated by a survival signaling pathway linked to NF- κ B, a major mediator of TFF-promoted cell survival. Besides that, the stable expression of a mutant form of the NF- κ B inhibitor (I- κ B) in cells resulted in a significant reduction against anoikis effect of TFF3 (Chen *et al.*, 2000). A study confirmed that TFF3 protected intestinal epithelial cells from anoikis (Regalo *et al.*, 2005) and induced oncogenic transformation of an normal immortalized human mammary epithelial cell line (Xu *et al.*, 2005). TFF3 over-expression in mammary carcinoma cells prevented tamoxifen-induced anoikis (Kannan *et al.*, 2010). Depleted expression of TFF3 inhibited anchorage-independent growth of human mammary carcinoma cells. Additionally, over-expression of TFF3 greatly enhanced colony formation in tamoxifen-resistant mammary carcinoma cells, while depleted expression of TFF3 restored sensitivity of tamoxifen-resistant cells to the same drug (Kannan *et al.*, 2010). Additionally, knockdown of TFF3 significantly inhibited colony formation of gastric carcinoma cells in soft agar (Chan *et al.*, 2005a) and suggesting that TFF3 prevents anokis.

(iv) Migration and invasion

One of the protective functions of the TFF peptides is to serve as motogens to assist in the restitution of damaged mucosal or epithelial tissue but this function may be co-opted in tumor metastasis to promote tumor cell migration and invasion. TFF3 and TFF1 are motogenic in both normal and cancer cells. TFF3 greatly promoted and enhanced migratory and invasive capacities of human colon carcinoma cells (Rivat *et al.*, 2005). Numerous studies have indicated over-expression of TFF3 to be involved in disrupting cell morphology and polarity in colon carcinoma cells by modulating the function of E-cadherin/catenin complex, which typically maintains normal cell to cell contacts (Efsthathiou *et al.*, 1998, Meyer zum Buschenfelde *et al.*, 2004). Disruption of these cell to cell contacts and cell polarity resulted in EMT associated with the stimulation of cellular invasion and migration in the metastasis of colon carcinoma cells (Meyer zum Buschenfelde *et al.*, 2004). TFF3 has been shown to promote migration and invasion by rat fibroblast cells by increased the expression of metalloproteinase-9 (MMP-9) and β -catenin as well as simultaneously decreased the expression of E-cadherin and tissue inhibitor of metalloproteinase-1 (TIMP-1) (Chan *et al.*, 2005b). Furthermore, the TFF3-mediated migration of normal and oncogenically transformed bronchial epithelial cells was demonstrated to be p44/42 MAPK-dependent (Graness *et al.*, 2002).

(v) Angiogenesis

Besides the functional role of TFF3 in resisting apoptosis and promoting cell invasion and migration, another oncogenic effect of TFF3 is the ability to promote angiogenesis, which is necessary for tumor growth and dissemination (Andre *et al.*, 2000). Physiological angiogenesis is fundamental in normal tissue homeostasis but this process is co-opted in tumorigenesis to promote survival and the growth of tumor. *In vitro* and *in vivo* studies have demonstrated that TFF peptides may serve as pro-angiogenic factors (Rodrigues *et al.*, 2003b, Emami *et al.*, 2004). Exogenous recombinant TFF protein (rhTFF1) promoted HUVEC tubule formation and the angiogenic responses of TFF1 similar to that observed with VEGF-A and

transforming growth factor- α . It has been shown that TFF1 was connected to the activation of VEGF receptor, cyclooxygenase (COX-2), and EGF-R pathways (Rodrigues *et al.*, 2003b). The expression of COX-2 greatly reduced apoptotic activity, increased tumor *de novo* angiogenesis, and promoted invasion and metastasis (Tsuji *et al.*, 1998). Nitric oxide (NO) is a growth factor for inflammation as well as tumor vascular formation (Tan *et al.*, 1999). Exogenous TFF3 has been reported to stimulate the formation of NO by inducing nitric oxide synthase for blood vessel formation (Rodrigues *et al.*, 2001). Concordantly, IHC analysis of gastric carcinoma tissues (Dhar *et al.*, 2005) and breast cancer tissue (Ahmed *et al.*, 2012) demonstrated that increased expression of TFF3 is significantly associated with enhanced tumor vascularity (Dhar *et al.*, 2005, Ahmed *et al.*, 2012).

1.3.8 Clinical correlation of TFF3 in mammary carcinoma

Mounting evidence has recently indicated a clinical association between the expression of TFF3 and the prognosis of breast cancer patient. It has been shown that increased expression of TFF1 and TFF3 mRNA were observed in lobular carcinoma *in situ*, invasive lobular carcinoma and invasive ductal carcinoma (Emami *et al.*, 2004). TFF3 mRNA has also been identified as a prognostic biomarker for breast cancers negative for both estrogen and progesterone receptor (Doane *et al.*, 2006). Kaplan-Meier analysis of breast cancer patients (ER+) treated with tamoxifen has demonstrated that elevated TFF3 mRNA expression is significantly associated with worse disease-free survival (Miller *et al.*, 2005, Kannan *et al.*, 2010). Concordantly, Kannan *et al.* (2010) observed a positive correlation between increased TFF3 mRNA expression and poor survival outcome not only in breast cancer patients but also patients treated with tamoxifen (Kannan *et al.*, 2010). IHC analysis of breast cancer tissues indicated that a negative association between TFF3 protein expression and labeling of cell proliferative biomarker Ki-67 (Ahmed *et al.*, 2012).

The pro-angiogenic function of TFF peptides has been demonstrated using recombinant TFF peptides to induce formation of tube-like structures by HUVEC in the

Matrigel matrix substratum, and capillary vessel formation in CAM assay (Rodrigues *et al.*, 2003b). Thus, the angiogenic activity of TFF peptides is comparable to that stimulated by VEGF and transforming growth factor- α . Furthermore, the association between the expression of TFF3 protein and microvessel density (measured by CD34 biomarker staining) has previously been reported in gastric carcinoma tissue (Dhar *et al.*, 2005). A recent cohort study on breast cancer patients, in which endothelial marker CD31 or CD34 expression were examined, has also shown a strong positive correlation between TFF3 protein expression and microvessel density, (Ahmed *et al.*, 2012).

TFF3 promotes invasive and metastatic phenotype in mammary carcinoma cells leading to tumor progression. During metastasis, TFF3 increases the penetration of neural sheath and the intravasation of lymphovasculture. The role of TFF3 protein expression in metastasis of breast cancer has not been extensively studied, but TFF1 and TFF3 mRNA had been identified as a marker for predicting micrometastatic breast cancer in a microarray analysis of early breast cancer patients (Mikhitarian *et al.*, 2005). Another array-based study has shown TFF1 and TFF3 to be two genes most highly and significantly associated with breast cancer metastatic to bone (Smid *et al.*, 2006). Concordantly, increased expression of TFF3 in mammary carcinoma cells was associated with invasive phenotype and metastatic potential, suggesting that continued involvement of TFF3 in the process of metastasis to facilitate the colonization of cancer cells in bone (Ahmed *et al.*, 2012). Additionally, the expression profiling of breast cancer was analyzed using serial analysis of gene expression (SAGE), indicating TFF1 and TFF3 to be signature targets that are expressed in mammary carcinoma and absent in the circulation and bone marrow (Bosma *et al.*, 2002). Therefore, TFF1 and TFF3 have been used as biomarkers for detecting disseminated breast cancer (Lacroix, 2006).

1.4 Angiogenesis

Angiogenesis is an essential process where new blood vessels are formed or new capillaries are grown from pre-existing vasculature (Folkman, 1971). This phenomenon is a tightly controlled and regulated event, which occurs in several normal physiological processes such as reproduction, growth and development, and wound repair (Folkman, 1971). However, angiogenesis can switch to a pathogenic process during tumor growth and metastasis as well as in other diseases such as atherosclerosis and endometriosis (Banerjee *et al.*, 2007).

The angiogenic process is pivotal in tumor growth whereby tumor progression highly dependent on blood vessel recruitment and tumors response to secretory angiogenic factors (Folkman *et al.*, 1971). Therefore, inhibition of tumor angiogenesis can be a potential therapeutic strategy to regress tumor growth (Folkman, 1971). In the past, many research studies related to tumor angiogenesis have been performed to prove that inhibition of angiogenesis could attenuate tumor growth. Recently, preclinical studies of angiogenesis inhibitors have shown that anti-angiogenic therapies may have great potential in the treatment of cancers (Tabruyn and Griffioen, 2007). The Food and Drug Administration (FDA) has approved several therapeutics strategies for the treatment of angiogenesis-dependent diseases including Avastin for colorectal cancer and Tarceva for lung cancer (Tabruyn and Griffioen, 2007).

1.4.1 Mechanism of angiogenesis

Both normal and cancer cells require adequate oxygen and nutrient supply, and the removal of waste products from metabolic processes and sustaining survival. Normally, cells and tissues depend on physiological vasculogenesis referred to as *de novo* angiogenesis to generate vasculature that can meet their metabolic demands (Papetti and Herman, 2002). Cancer cells initially supply their own oxygen and nutrients from the pre-existing vasculature by mimicking normal angiogenesis. Consequently, tumors remain dormant and still able to

survive through the pre-existing vasculature and may not need to induce tumor angiogenesis (Holash *et al.*, 1999).

Tumor angiogenesis is a pathological event resulting from the use of normal angiogenic mechanism, where vasculature is remodeled by new capillaries formation from pre-existing vessels (Papetti and Herman, 2002). Normal angiogenesis provides an adequate source of oxygen and nutrients to the developing or healing tissues. Within a tumor, there is limited amount of nutrients available for actively dividing cells (Folkman, 1971, Jain, 1987). Consequently, tumor cells induce development of new vessels from pre-established vasculature, thereby producing a vascular network that delivers oxygen and nutrients for survival and propagation of tumor cells.

In the physiological angiogenesis, new vessels develop regularly from normal vasculature comprised of mature vessels and maintained by the combination of pro- and anti-angiogenic molecules (Jain, 2001). Endothelial cells (EC) are among the more quiescent and genetically stable cells in the body. Unlike normal blood vessels, tumor vessels generated in pathological angiogenesis are structurally and functionally abnormal. Characteristics of tumor angiogenesis include the presence of highly proliferative EC and atypical morphology of the intratumoral vasculature (Rajotte *et al.*, 1998). The hierarchy of capillaries, arterioles, and venules which is characteristics of normal vasculature is distorted in tumors (Baish and Jain, 2000). EC, pericytes and smooth muscle cells, and the basement membrane of tumor blood vessels are poorly organized (Baluk *et al.*, 2005). Under normal circumstances, EC do not associate with normal blood vessel. However, vasculature produced during tumor angiogenesis becomes hyperpermeable and poorly organized that generally results in high interstitial pressure in most tumors (Baluk *et al.*, 2005). In addition, pericytes are not tightly attached to EC and the vessel wall may weaken and increase the risk of metastasis of cancer cells (Baish and Jain, 2000).

The angiogenic event is highly toned by combination of pro-angiogenic and anti-angiogenic factors (Huang and Bao, 2004, Adams and Alitalo, 2007). An imbalance of either

pro- and anti-angiogenic factors will thus trigger the tumor angiogenesis cascade. When the angiogenic state is favorable, new blood vessel is formed with activation of EC and the removal of mural cells (pericytes) from pre-established vasculature (Figure 15). The absence of these pericytes initiates MMPs to proteolytically degrade the basement membrane of the vasculature (VBM) and ECM (Moses, 1997). The growth of endothelial sprouts (also known as angiogenic sprouting) from pre-existing blood vessel requires a change of cell polarity, induction of motility and invasive capacity, the decrease of cell-cell contact and the degradation of the ECM. Angiogenic sprouting is then followed by an outgrowth of EC, which is regulated by a gradient of pro-angiogenic factors such as VEGF-A. These pro-angiogenic factors are released or produced by VBM and a variety of cell types including tumor cells, fibroblasts, and immune cells. The EC continue to proliferate until they start to form microvessel. After formation of the small blood vessel, recruitment of mesenchymal cells to the vessels occurs, where the cells subsequently differentiated into pericytes and the cell to cell connections between pericytes and EC is substantially established. Finally, the development of stable and mature blood vessels terminates the process. The cells differentiate in a structure identical to capillaries in order to create a vascular network and blood flow that is crucial for cancer development (Adams and Alitalo, 2007).

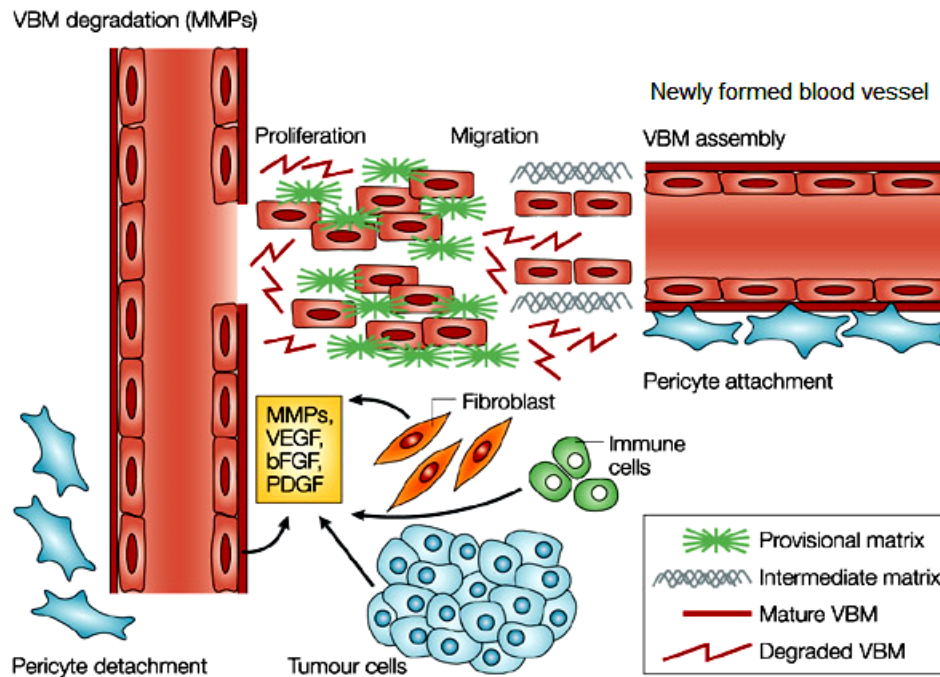


Figure 15: Tumor angiogenesis cascade. Tumor angiogenesis involved degradation and reformation of the vascular basement membrane (VBM). Basement membrane, fibroblasts and immune cells, and tumor cells release a variety of pro-angiogenic factors, such as vascular endothelial growth factor (VEGF). Pro-angiogenic factors and matrix metalloproteinases (MMPs) stimulate structural changes and degradation of basement membrane. These angiogenic factors also induce recruitment of pericytes to stabilize the newly formed blood vessels (Nussenbaum and Herman, 2010).

1.4.2 Angiogenesis and tumor progression

Angiogenesis may influence the ability of tumor outgrowth and metastasis (Folkman *et al.*, 1971). Folkman *et al.* (1971) first discovered the effect of angiogenic factors in tumor progression and also reported the induction of angiogenesis by angiogenic factors secreted from tumor cells. Tumor cells require diffusion of nutrient supply from the interstitial space in the absence of angiogenic factors where tumor usually do not grow beyond 3 - 4 mm in diameter (Folkman, 1990). Laboratory experiments have been done to prove that tumors release angiogenic factors by transplantation of melanoma (Greenblatt and Shubi, 1968) or choriocarcinoma cells (Ehrmann and Knoth, 1968) and that blood vessel proliferation was promoted even in the presence of a filter barrier between host and tumor. These findings support that tumor angiogenesis is promoted by angiogenic factors that are synthesized by

tumor cells. In the absence of vascular support, tumors are restricted with an inadequate supply of oxygen and nutrient and undergo necrosis or apoptosis. Consequently, tumor growth is reduced or remains dormant (Holmgren *et al.*, 1995, Parangi *et al.*, 1996). To overcome this condition, tumor cells induce formation of capillaries by splitting from the original vessel (Carmeliet and Jain, 2000). Tumor angiogenesis significantly contributes to tumor progression by supplying nutrients and oxygen crucial for cancer growth as well as providing a route for dissemination of tumor cells through the bloodstream to secondary organs and form metastases (Cao, 2005).

The process of “angiogenic switch” describes the process of transition from a pre-vascular hyperplasia to a highly vascularized tumor. It is highly regulated by the fine-tuned equilibrium between pro- and anti-angiogenic factors released from tumor cells and/or stromal cells in tumor interstitium (Bergers and Benjamin, 2003). The production of pro-angiogenic factors are also influenced by external factors such as glucose deprivation, cellular acidosis, hypoxia or by deregulation of oncogenes or tumor suppressor genes (Arbiser *et al.*, 1997, Pugh and Ratcliffe, 2003, North *et al.*, 2005). The equilibrium between pro- and anti-angiogenic function prevents tumor outgrowth, which is known as tumor dormancy (Gelao *et al.*, 2013). The shift in equilibrium towards pro-angiogenic functions is associated with tumor and subsequently dissemination of tumors (Gelao *et al.*, 2013) (Figure 16).

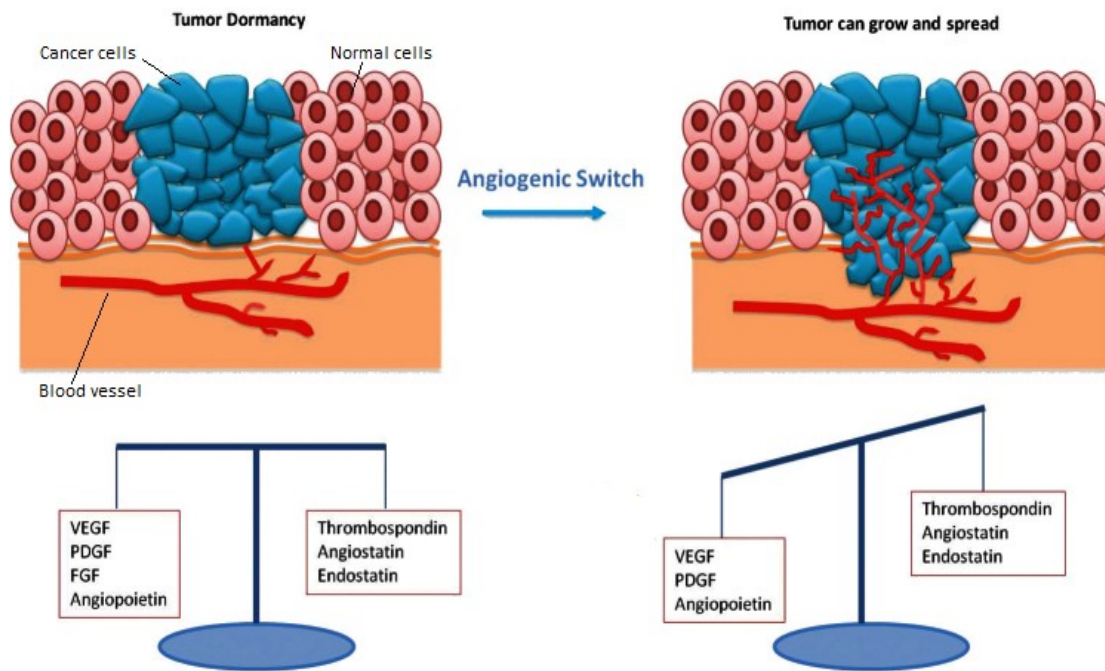


Figure 16: Angiogenic factors in tumor dormancy and growth. An equilibrium between pro-angiogenic and anti-angiogenic factors is found in the tumor dormancy. When this equilibrium is distorted by the prevalence of pro-angiogenic factors, tumor can grow and spread (Gelao *et al.*, 2013).

The angiogenic switch can take place at different stages during tumor progression based on the specific characteristics of the tumor as well as the tumor interstitium (Figure 17). Majority of tumors begin growing as avascular nodules. The angiogenic switch that favors tumor angiogenesis is required to ensure exponential tumor growth. Tumor angiogenesis process involves perivascular detachment, recruitment of EC, activation of EC by angiogenic factors, angiogenic sprouting, stabilization new vessels by perivascular and finally vasculature formation (Cameron *et al.*, 2005). This blood vessel formation allows nutrients to be delivered to hypoxic cells and to the necrotic areas of the tumor for tumor growth and expansion (Bergers and Benjamin, 2003). Therefore, the effect of angiogenic factors secreted by tumor and the regulatory molecules in ECM as well as proteolytic activities in ECM remodeling within the tumor interstitium may contribute to tumor angiogenesis for disseminating cancer cells to distant organs (Mott *et al.* 2004; Sottile 2004).

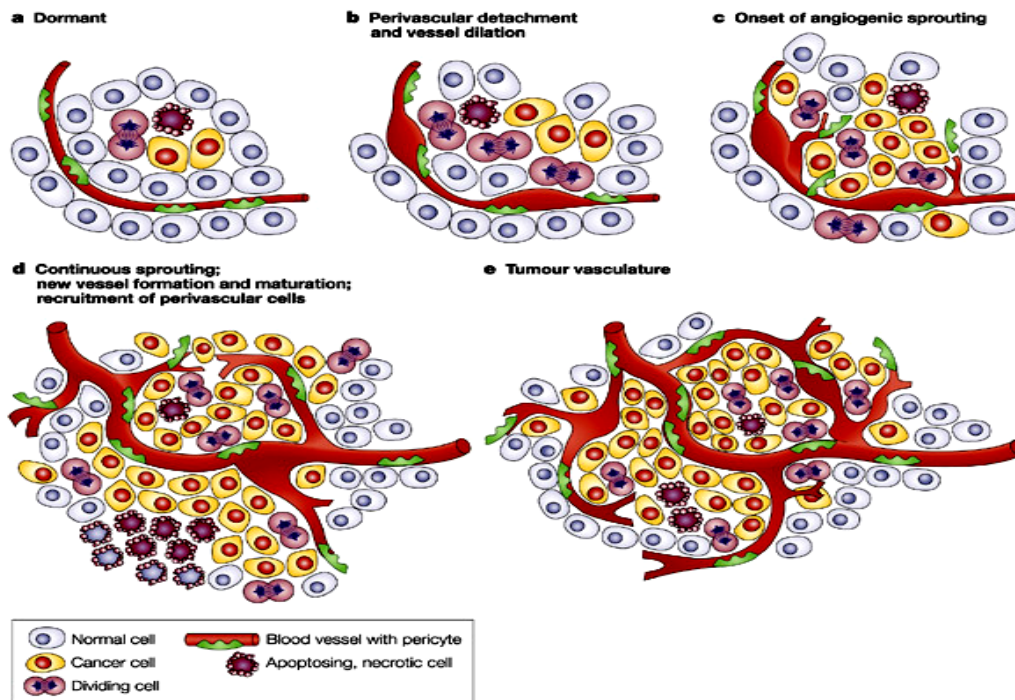


Figure 17: Angiogenic switch and the process of pathological angiogenesis in tumor progression. The angiogenic switch is a distinct step in tumor development that can occur at different stages in the process of tumor progression. a, tumor begins as an avascular masses (dormant). b, the 'angiogenic switch' has to occur to promote tumor growth. The switch started with perivascular detachment and vessel dilation. c, angiogenic sprouting. d, new vessel formation and maturation. e, formation of vasculature in tumor to supply oxygen and nutrient to the cancer cells (Bergers and Benjamin, 2003). Reproduced with permission.

1.4.3 Regulators of angiogenesis

Regulators of angiogenesis are secreted from various cell types such as immune cells, tumor cells and stromal cells or (Folkman, 2003). In normal tissues, anti-angiogenic factors are in excess and maintain the tissue vascularization in a quiescent state. Tumor angiogenesis results from the up-regulation of pro-angiogenic factors and the down-regulation of normal expression level of anti-angiogenic factors (Hanahan *et al.* 1996; Sund *et al.* 2005).

Tumor cells produce many angiogenic factors to induce endothelial cells proliferation and differentiation. Example of angiogenic factors includes interleukin-8 (IL-8), VEGF-A, platelet-derived growth factor (PDGF), angiopoietins (Ang), acidic and basic fibroblast growth factor (aFGF and bFGF) (Folkman 2003). Among these, IL-8 and VEGF-A are the most pivotal regulators of angiogenesis (Ferrara *et al.*, 2003). FGF and PDGF induce EC

proliferation and migration by interaction with cognate receptors in the EC (Battegay *et al.*, 1994, Friesel and Maciag, 1995). Ang promotes sprouting of vascular remodeling and angiogenesis. Ang-1 promotes the maturation of blood vessel and thus inhibits angiogenesis. Ang-2 antagonizes Ang-1 activity and allows the growing blood vessel to be more responsive to additional angiogenic factors stimulation (Augustin *et al.*, 2009).

Angiogenesis is inhibited by anti-angiogenic factors such as thrombospondins (Tsp), endostatin, angiostatin, interferon- α and - β (INF- α and - β) (Huang and Bao, 2004). TSP-1 is a large ECM glycoprotein and proteolytic fragments (Good *et al.*, 1990). TSP-1 directly inhibits angiogenesis by decreasing EC migration and survival or through indirect action of TSP-1 molecules on activation of transforming growth factor (TGF) and matrix metalloproteinases (MMPs) to inhibit tumor growth (Lawler, 2002, Huang and Bao, 2004). Endostatin is produced by cleavage of collagen XVIII (O'Reilly *et al.*, 1994). Endostatin stabilizes newly formed endothelial tubes in the regions of the tumor where new blood vessel formation is occurring that specifically inhibits endothelial proliferation and tumor growth (Li *et al.*, 2003b). Finally, angiostatin is a fragment of plasminogen and has been demonstrated to be an inhibitor of both neovascularization and additionally metastatic dissemination (O'Reilly *et al.*, 1994). Thereby, the genetic and additional epigenetic events within the tumor interact with the cocktail of pro- and anti-angiogenic factors to induce an angiogenic phenotype in tumor cells (Hanahan *et al.* 1996) and thus initiate tumor angiogenesis.

1.4.4 Vascular Endothelial Growth Factor A (VEGF-A)

VEGF-A is an angiogenic-promoting protein that has a pivotal role in regulating physiological and pathological angiogenesis. It is a member of the VEGF family comprise of seven members: VEGF-A, VEGF-B, VEGF-C, VEGF-D, VEGF-E, VEGF-F, and PlGF. The members possess a VEGF homology domain and bind to their tyrosine kinase receptors, VEGFR-1, -2, and -3 (Ferrara *et al.*, 2003). VEGF-A is known as a tumor-produced cytokine and is implicated in normal tissue and tumor-associated angiogenesis. It promotes

proliferation and tube formation in endothelial cells (Ferrara *et al.*, 2003, Rini and Small, 2005). The VEGF gene is located on the short arm of chromosome 6 containing eight exons and may be differentially spliced to produce four mature isoforms (VEGF₁₂₁, VEGF₁₆₅, VEGF₁₈₉ and VEGF₂₀₆) (Holmes and Zachary, 2005). Other isoforms were later recognized such as VEGF₁₄₅ and VEGF₁₈₃ (Tischer *et al.*, 1991). VEGF₁₆₅ is identified as the most predominant isoforms and is overly expressed in a variety of solid tumors. It is a potent angiogenic factor for tumor vascularization (Nishi *et al.*, 2005). VEGF-A exerts its biologic function by interacting with cell surface tyrosine kinase receptors consists of VEGFR-1/Flt-1 and VEGFR-2/Flk-1 expressed on the endothelial cells and neuropilin receptors (NP-1 and NP-2) expressed in the vascular endothelium (Dvorak, 2002). When VEGF-A binds its receptor, a number of downstream pathways are activated upon receptor dimerization and autophosphorylation of the intracellular tyrosine kinase domains (Ferrara *et al.*, 2003). VEGFR-2 was found to be the main receptor mediating the pro-angiogenic effects of VEGF-A (Ferrara *et al.*, 2003). Related molecules include VEGF-D and VEGF-C which are structurally similar, but are less homologous VEGF-A (Robinson and Stringer, 2001). These factors preferentially activate VEGFR-3 present predominantly on lymphatic EC and therefore promote lymphangiogenesis (Alitalo *et al.*, 2005). Experimental studies on mouse models have demonstrated that inhibiting the biological functions of VEGF-A with adenoviral delivery of a soluble form of VEGFR-1/2, by depletion of VEGF-A, and by the use of a chemical inhibitor of VEGF signaling impaired tumor angiogenesis and growth (Vajkoczy *et al.*, 1999, Inoue *et al.*, 2002, Casanovas *et al.*, 2005).

1.4.5 Interleukin-8 (IL-8)

Interleukin-8 is a member of the chemokine family, which is specific cytokines secreted by both normal cells and cancer cells. Generally, secretion of this cytokines is dependent on growth factors, inflammatory cytokines, and pathophysiological conditions (Koch *et al.*, 1992, Strieter *et al.*, 1992). IL-8 is known as a chemotactic protein secreted by

macrophages and activated monocytes that function to promote the directional migration of T lymphocytes, basophils, and neutrophils (Zlotnik and Yoshie, 2000). IL-8 possesses important functions in infectious diseases, autoimmune, and inflammatory (Koch *et al.*, 1992, Harada *et al.*, 1994). Due to strong inflammatory properties, IL-8 expression is controlled tightly with undetectable or low expression under normal circumstances. Over-expression of IL-8 has been demonstrated in a number of human cancers including those of melanoma, breast, and ovarian (Xu and Fidler, 2000, Freund *et al.*, 2003, Singh *et al.*, 2010). IL-8 plays a crucial role in angiogenesis in both physiologic and pathological conditions (Koch *et al.*, 1992, Strieter *et al.*, 1995a). Previous studies showed that IL-8 promoted tumor growth and increased metastatic potential of cancer cells (Miller *et al.*, 1998, Gomperts and Strieter, 2006). Additionally, IL-8 exhibited profound roles in tumor progression due to its ability to affect different cell of the tumor microenvironment (Xie, 2001, Waugh and Wilson, 2008).

(i) IL-8 structure

IL-8 is a small peptide (8 - 10 kDa), belonging to the CXC chemokine family and secreted by stromal (endothelial cells and fibroblasts) and tumor cells. The CXC chemokine family is further categorized based on conserved cysteines within the N-terminal amino acid sequence (Baggiolini *et al.*, 1997) as well as absence or presence of a three amino acid sequence, glutamic acid-leucine-arginine (ELR motif) which precedes the first cysteine residue in the CXC sequence. The ELR motif is important because the ELR (containing ELR+) CXC chemokines are potent promoters of angiogenesis and on the contrary, non-ELR (containing ELR-) CXC chemokines are anti-angiogenic (Strieter *et al.*, 1995a). Among these (ELR+) CXC chemokines, IL-8 is a potent angiogenic-promoting factor that stimulates formation of blood vessel in tumors. IL-8 gene is clustered on chromosome 4 between 4q12 and 4q21, consisting sequence identity between 24% to 46% with other CXC family members (Brat *et al.*, 2005). Transcription of the IL-8 gene produces a 99 amino acids protein which is processed through post-translational modification to yield two biological active IL-8 isoforms, with peptides of 72 and 77 amino acid residues (Hébert and Baker, 1993). The 72 amino acid

peptide is secreted by monocytes and macrophages. The 77 amino acid variant is the most abundant isoform of non-immune cells. The peptide structure of IL-8 is monomeric and composed of an NH₂-terminal loop that is important for receptor activation, a central three anti-parallel beta sheet-strands connected by loops that provides a stable scaffold, and a C-terminal alpha helix that stabilizes the overall structure by folding over the small beta-sheet (Figure 18). IL-8 forms dimers although the monomer is a prevalent and active moiety of this chemokine (Rajaratnam *et al.*, 1994, Horcher *et al.*, 1998). Experimental data has demonstrated that IL-8 binds to its receptor N-domain as a monomer (Lowman *et al.*, 1997, Fernando *et al.*, 2004).

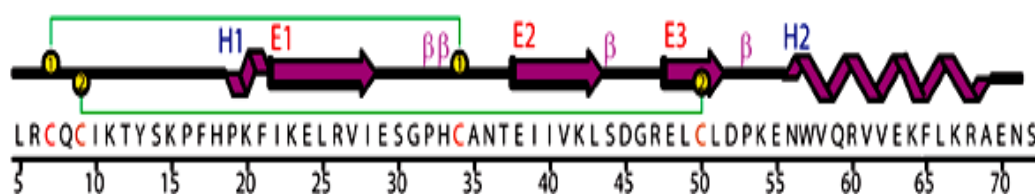


Figure 18: Primary structures of IL-8. Primary structure for interleukin-8 (PDB code: 3IL8). The N-terminal loop, which is responsible for receptor recognition, is restrained by two disulfide bonds. This is followed by a short turn of a 3_{10} helix (H1) that leads to a three-stranded anti-parallel β -sheet. The C-terminal α -helix folds over the β -sheet (H2) and helps to stabilize the overall tertiary structure (Kanagarajadurai and Sowdhamini, 2008).

The regulatory sequences have been categorized from -1 to -2500 bp of the 5'-flanking region of the IL-8 gene. One of the most characterized regions occurs at -425 to -70 bp and which possesses binding sites for the transcription factors C-EBP/NF-IL-6, AP-1, and NF- κ B, as well as potential binding sites for the interferon regulatory factor-1, glucocorticoid receptor, and hepatocyte nuclear factor-1 (Mukaida *et al.*, 1994, Hoffmann *et al.*, 2002) (Figure 19). A recent study has identified a putative STAT3 binding site that positioned from -245 to -237 bp in the IL-8 promoter region (Oka *et al.*, 2010). Additionally, the estrogen response elements and C-EBP/NF-IL-6 consensus sites have been identified in the IL-8 promoter, and are involved in the activation of IL-8 production (Mukaida *et al.*, 1994,

Roebuck, 1999). NF- κ B binding is required for promotion of IL-8 promoter activity (Matsusaka *et al.*, 1993). C-EBP/NF-IL-6 and AP-1 may contribute to transcriptional activity but dependent on the particular cell type (Mukaida *et al.*, 1990). Additionally, the expression of IL-8 is partially regulated by other stimuli such as environmental stresses (e.g., exposure to chemotherapy agents and hypoxia), chemical and steroid hormones, and inflammatory signals (e.g., tumor necrosis factor α) (Brat *et al.*, 2005).

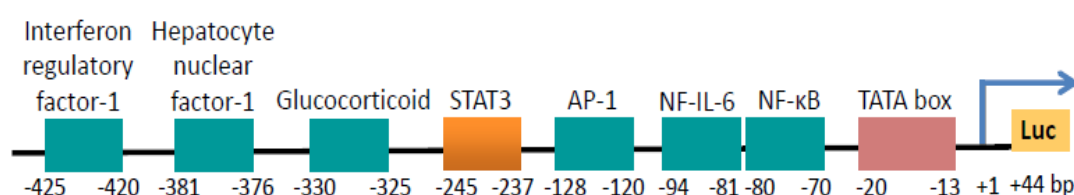


Figure 19: Binding sites for transcriptional factors in IL-8 promoter region. The consensus DNA-binding sites for known transcription factors in the promoter region of IL-8 gene. The putative STAT3 binding site is positioned from - 245 to -237 bp in the IL-8 promoter (Oka *et al.*, 2010). Adapted from Oka *et al.*, 2010.

(ii) Roles of IL-8 and its cognate receptors in tumor microenvironment

The biological roles of IL-8 are produced by two different G protein–coupled receptors, termed as CXCR1 and CXCR2. IL-8 binds CXCR1 and/or CXCR2, with the same affinity, and thereby activates downstream signaling cascades that regulate cellular function (Murphy and Tiffany, 1991). CXCR1 and/or CXCR2 are known to be the only mammalian receptors of IL-8 with the specific amino acid sequence of ELR motif at the N-domain. CXCR1 receptor is activated solely in response to IL-8 but may also be activated by granulocyte chemotactic protein-2. Alternatively, activation of CXCR2 requires multiple CXC chemokines including neutrophil-activating peptide, growth-related oncogenes (GRO α , β , and γ), and granulocyte chemotactic protein-2. They share 78% amino acid sequence homology and are also considered biologically active IL-8 cognate receptors (Ahuja and Murphy, 1996). The CXCR1 and CXCR2 receptors are highly expressed in neutrophils/tumor-associated macrophages, endothelial cells, and cancer cells. Multiple

reports have demonstrated that the over-expression of IL-8 by cancer cells was promoted by chemotherapeutic treatment or environmental stresses such as hypoxia. The increased synthesis and secretion of IL-8 from tumor cells exert profound effects on the tumor microenvironment (Figure 20). IL-8 secreted from cancer cells promotes cellular proliferation and survival. Additionally, IL-8 activates endothelial cells in tumor vasculature to stimulate *de novo* angiogenesis and promote chemotactic infiltration of neutrophils into the tumor. In addition to its capacity to promote cell invasion and migration, IL-8 also induces tumor-associated macrophages to secrete other growth factors to enhance cancer cell proliferation and invasion within the tumor (Waugh *et al.* 2008). Activation of IL-8 downstream signaling pathways include PI3K/Akt, Src-kinases and FAK, and MAPK signaling cascades, resulting in enhanced transcriptional activity of the signaling proteins implicated in angiogenesis, proliferation, migration and invasion (Todorović-Raković and Milovanović, 2013).

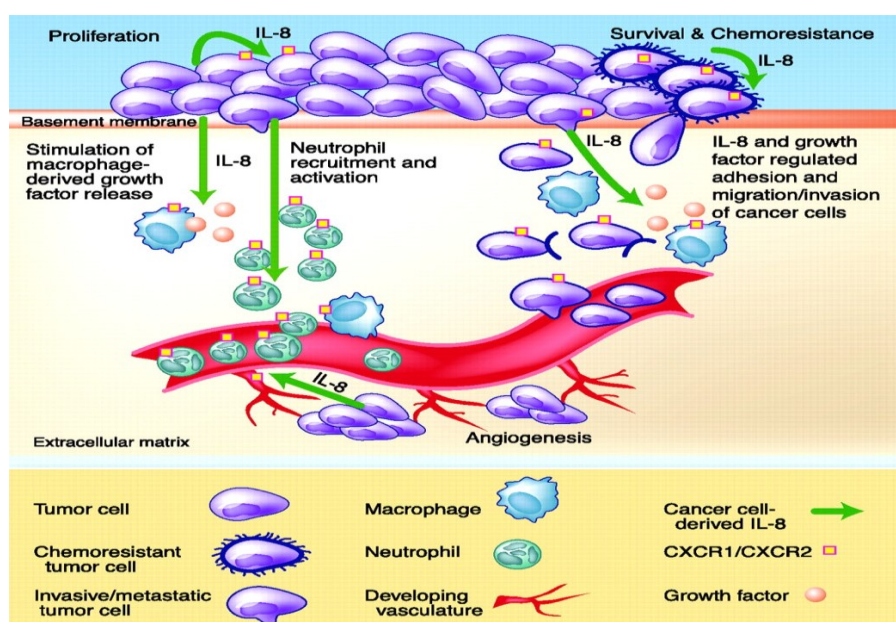


Figure 20: The role of IL-8 signaling in the tumor microenvironment. Tumor-derived IL-8 is able to exert profound effects on the tumor microenvironment. Secretion of IL-8 from cancer cells can enhance the proliferation and survival of cancer cells through autocrine signalling manner. In addition, tumor-derived IL-8 will activate endothelial cells in the tumor vasculature to promote angiogenesis and induce a chemotactic infiltration of neutrophils into the tumor site. IL-8 also stimulates tumor-associated macrophages to release growth factors for cancer cell migration and invasion (Waugh and Wilson, 2008). Reproduced with permission.

(iii) Biological effects of IL-8 in tumor angiogenesis and metastasis

IL-8 has an autocrine and/or paracrine tumor-promoting role in modulating the survival and proliferation of tumor cells. The biological activity of IL-8 in tumors and the tumor microenvironment may contribute to tumor progression through leukocyte infiltration, stimulation of cancer cell motility, angiogenesis, cancer cell growth and survival (Yuan *et al.*, 2005). Accordingly, Ewington *et al.* (2012) has recently demonstrated that the pathogenesis of endometrial carcinoma was positively associated with the expression of IL-8 and/or its cognate receptors (Ewington *et al.*, 2012). Additionally, Nastase *et al.* (2011) has suggested that IL-8 is useful to diagnose early stage colon cancer and to monitor the progression of colon tumors (Nastase *et al.*, 2011). The expression of IL-8 and IL-8 receptors in melanoma was shown to be positively correlated with disease progression (Singh *et al.*, 2010). Increased the expression of IL-8 and IL-8 receptors is associated with worse prognosis in breast cancer patients, indicating that the metastatic capacity of breast cancer cells was strongly correlated with the expression level of IL-8 (Miller *et al.*, 1998, De Larco *et al.*, 2001). Furthermore, a study has suggested that polymorphism of IL-8 and CXCR2 genes in breast cancer, which modulates the expression of IL-8 could promote tumor progression in breast cancer (Snoussi *et al.*, 2010). It has been reported that the effect of sex steroid in the regulation of IL-8 is contradicting and apparently varies in different tissues (Kanda and Watanabe, 2001, Bengtsson *et al.*, 2004). Increased IL-8 expression was observed in ER- breast cancer cells (MDA-MB-231) as compared to ER+ breast cancer cells (MCF-7) (Freund *et al.*, 2003, Lin *et al.*, 2004). Estrogen did not affect IL-8 expression in ER- or ER+ breast cancer cells, whereas it strongly induced TFF1 expression (a marker of estrogen responsiveness) in ER+ breast cancer cells. These observations support that the expression of IL-8 is associated with a higher invasiveness potential of cancer cells *in vitro* and therefore confirming the invasion-promoting effect of IL-8 (Freund *et al.*, 2003).

IL-8 plays a direct role in angiogenesis by promoting endothelial cell proliferation and survival as well as stimulating the expression of matrix metalloproteinase in endothelial

cells expressing CXCR1 and CXCR2 (Li *et al.*, 2003a). IL-8 stimulates endothelial proliferation and also capillary tube formation and these effects are inhibited by monoclonal antibodies to IL-8. A recent report has demonstrated that IL-8 stimulated VEGF A expression in endothelial cells via CXCR2, and hence increased the activation of VEGF receptors in an autocrine manner (Martin *et al.*, 2009). Moreover, IL-8 has been shown to enhance secretion of matrix metalloproteinase MMP-2 and MMP-9, suggesting that IL-8 can modulate invasiveness and/or ECM remodeling in the tumor microenvironment (Inoue *et al.*, 2000a, Inoue *et al.*, 2000b). As processes such as migration, cell proliferation, invasion, and angiogenesis are involved in metastasis, IL-8 expression by tumor cells can therefore have an effect on their metastatic capabilities. The expression of IL-8 is reported to correlate with the metastatic potential of cancer cells. The highly metastatic melanoma cells expressed higher level of IL-8 mRNA than melanoma cells with low metastatic capacity, suggesting that increased IL-8 mRNA expression is associated with the metastatic potential of cancer cells (Singh and Lokeshwar, 2009). Increased IL-8 in the tumor interstitium was shown to promote colon cancer growth and metastasis (Lee *et al.*, 2012). Conversely, the growth of colon cancer is prevented by the absence of its receptor CXCR2 in the tumor microenvironment (Lee *et al.*, 2012). In xenograft model, colon cancer cells expressing IL-8 formed significantly larger tumors with increased microvessel density when compared with the control cells (Ning *et al.*, 2011). Increased IL-8 expression promotes invasion and angiogenesis of breast cancer cells (Lin *et al.*, 2004). Additionally, over-expression of IL-8 in non-metastatic melanoma cells enhanced their invasion through Matrigel-coated filters and produced highly malignant and metastatic neoplasms in mice models (Kitadai *et al.*, 1999). When gastric carcinoma cells that secrete low levels of IL-8 protein were stably transfected with a IL-8 gene, the transfected cells produced more rapidly growing, highly vascular neoplasms as compared with the control cells (Kanayama *et al.*, 1999). Furthermore, treatment of HUVEC with conditioned medium from the IL-8 expressing cells stimulated HUVEC proliferation, suggesting that IL-8 is

pivotal in promoting endothelial cell proliferation and tumor vasculogenesis (Beierle *et al.*, 2001).

Accumulating clinical studies have reported that IL-8 expression to be associated with the advanced stages of cancers and therefore suppressing the effects of IL-8 has important clinical implications for tumor progression. Neutralizing antibodies to IL-8 receptors, humanized antibody against IL-8, small molecule IL-8 receptor inhibitor and repertaxin have already been employed in preclinical studies, where their ability to inhibit angiogenesis, tumor growth, and metastasis of various xenograft tumor models have been demonstrated (Ginestier *et al.*, 2010).

1.4.6 Lymphangiogenesis

Although both the blood and lymphatic systems have been implicated in metastasis, preclinical experimental data suggest that the majority of initial metastasis site is via the lymphatic (Stacker *et al.*, 2002, Sleeman and Thiele, 2009). Clinical evidence has also demonstrated that lymphatic vessel density, both in and around the tumors, was significantly associated with lymphatic metastasis and also worse survival outcomes (Ran *et al.*, 2010). Lymphangiogenesis is implicated in some of the physiological processes such as homeostasis, metabolism and immunity. In contrast, regional lymph node metastasis is common in cancer and is utilized as a marker for tumor dissemination, stage, and prognosis (Sundar and Ganesan, 2007). Migration of cancer cells to regional lymph nodes is enhanced by lymphangiogenesis, a process in which lymphatic vessels are generated from pre-existing lymphatics (Ran *et al.*, 2010). Lymphangiogenesis is a complex and coordinated process to induce proliferation, migration and tube formation as is observed in tumor angiogenesis (Sundar and Ganesan, 2007, Ran *et al.*, 2010). Lymphangiogenic factors are often expressed in tumor-infiltrating and stromal cells, promoting optimal conditions for production of new lymphatic vessels. The most crucial lymphangiogenic factor that induces lymphangiogenesis is VEGFR-3, which is activated by VEGF-C and VEGF-D. Experimental studies have

demonstrated that VEGF-C/VEGF-D/VEGFR-3 signaling can promote lymphangiogenesis and dissemination from the primary tumor (Achen *et al.*, 2006). VEGFR3 expression is confined to lymphatic EC and facilitates the actions of VEGF-C and D (Shibuya and Claesson-Welsh, 2006). VEGF-C and -D are the most predominant growth factors in regulating this process (Nagy *et al.*, 2002, Bjorndahl *et al.*, 2005). Cancer cells potentially utilized the same chemokine ligands and its chemokine receptors for metastasis (Muller *et al.*, 2001). For example, human mammary carcinoma expressed chemokine receptors CXCR4 and CCR7, and their respective receptor CCL21 (secondary lymphoid chemokine) and CXCL12 (stromal-cell derived factor 1) are highly expressed in the target organs of metastasis (Muller *et al.*, 2001). Similarly, lymphatic EC synthesized chemokine CCL21, which activates CCR7 leading to chemoattraction and migration to lymph nodes. Breast cancer which expresses CXCR4 or CCR7 exhibit enhanced lymphatic metastasis as a consequence of chemoattraction and directional migration toward the ligand over-expressing lymph nodes (Ran *et al.*, 2010). Similar to angiogenesis, lymphangiogenesis promotes tumor metastasis.

1.4.7 Clinical implications on angiogenesis therapy

As angiogenesis is important and critical for cancer growth and metastasis, it is therefore a promising approach in controlling or limiting cancer progression (Weis and Cheresh, 2011). The association of the VEGF-A/VEGFR-2 signaling pathway as a pivotal regulator of tumor angiogenesis has resulted in generation of angiogenesis inhibitors against VEGF-A-mediated signal transduction. Some of the angiogenesis inhibitors have been approved for clinical use in cancer treatment. (Ellis and Hicklin, 2008).

Angiogenesis inhibitors can be defined as direct and indirect inhibitors. Direct angiogenesis inhibitors act directly on the tumor-derived endothelial cells by inhibiting their proliferation and migration. Indirect angiogenesis inhibitors are used to block the angiogenic factors and/or pathways that promote angiogenesis (Gasparini *et al.*, 2005). The indirect angiogenesis inhibitors that directly target VEGF-A, include Iressa (tyrosine kinase inhibitor),

Avastin or Bevacizumab (humanized anti-VEGF-A monoclonal antibody) and SU11248 (VEGF receptor blocking agent). In contrast, direct angiogenesis inhibitors abrogate the vascular endothelial cell proliferation, migration and/or resistance to apoptosis when in the presence of angiogenic proteins (Kerbel *et al.*, 2002). Angiogenic inhibitors such as endostatin also directly targets microvascular endothelial cells by preventing stimulation of angiogenesis-promoting factors (Kerbel *et al.*, 2002, Folkman, 2003). Depending on cancer type, treatment against angiogenesis may produce 3 - 6 months increase in patient progression-free survival. However, these angiogenic therapies may not provide enduring therapeutic efficacy, and confer only transitory clinical benefits to cancer patients. In these patients, revascularization may occur followed by enhanced metastasis (Baeriswyl and Christofori, 2009, Paez-Ribes *et al.*, 2009) (Figure 21). More importantly, inhibition of VEGF-A function may produce hypoxia-mediated increases in FGF expression to restart angiogenesis and tumor growth. Concomitant blockade of VEGF and FGF signaling, however, impeded the adaptive resistance to anti-angiogenic therapy of VEGF (Casanovas *et al.*, 2005). Hence, the emergence of resistance against anti-angiogenic therapies could be prevented by other angiogenic pathways stimulated as a compensatory mechanism (Hilberg *et al.*, 2008).

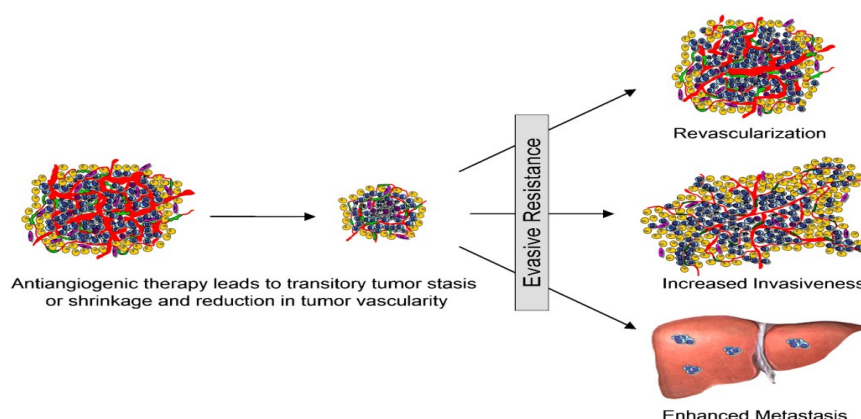


Figure 21: Adaptive resistance to anti-angiogenic therapies in cancers. Anti-angiogenic therapies produce transitory tumors shrinkage and reduction in tumor angiogenesis. Tumors subsequently are adapted to the angiogenic inhibitors. The emergent mechanisms of evasive resistance in tumors include revascularization via alternative pro-angiogenic signals, increased local invasiveness, and/or enhanced distant metastasis (Paez-Ribes *et al.*, 2009). Reproduced with permission.

1.5 Rationale and objectives of this study

Mounting evidence has shown that TFF3 protein is over-expressed in human mammary carcinoma where it is normally localized in mammary epithelial cells, suggesting that TFF3 exerts oncogenic effect on tumor growth and progression (May and Westley, 1997a, Poulsom *et al.*, 1997). TFF3 functions as a pro-survival and pro-invasive factor in mammary carcinoma (Emami *et al.*, 2001, Kannan *et al.*, 2010). Exogenous recombinant TFF3 induced HUVEC tubule formation *in vitro* (Rodrigues *et al.*, 2003b). The biological effects of TFF3 in the progression of mammary carcinoma have been extensively studied. However, the potential angiogenic effect of TFF3 has not been defined with the underlying mechanism is still not yet fully delineated. I propose that TFF3 promotes angiogenesis in mammary carcinoma and that underlying mechanism of TFF3 may involve modulation of targeted angiogenic factors and its transcription factors. The aims of this study are to investigate the stimulatory effects of TFF3 secreted from mammary carcinoma cells on the angiogenic activities of HUVEC as well as to delineate the mechanism of TFF3 in mammary carcinoma angiogenesis. The objectives of this study are:

1. To define the functional effects of TFF3 secreted from mammary carcinoma cells on the angiogenic behaviors of HUVEC;
2. To determine the *in vivo* angiogenic effect of TFF3 to stimulate microvessel density in mammary carcinoma cells-derived xenograft;
3. To identify the TFF3-stimulated angiogenic factors and the underlying mechanism of TFF3 in mammary carcinoma angiogenesis;
4. To determine the exogenous recombinant human TFF3 (rhTFF3) stimulation on the angiogenic behaviors of HUVEC; and
5. To define the functional effects of TFF3 secreted from HUVEC on the angiogenic behaviors of HUVEC

CHAPTER 2

Materials and Methods

2.1 Materials

The list of chemicals and reagents were enlisted in Table 1. The formulations and compositions of media, solutions, and buffers were also outlined in the Appendices. All water was purified through a Milli-Q purification system (Millipore Corporation, Billerica, MA, USA) and solutions were either autoclaved or filtrated through a 0.2 µm membrane.

Table 1: Chemicals and reagents

Chemicals and reagents	Source
100 bp or 1kb plus DNA ladder	Promega Corporation, Madison, WI, USA
10x Trypsin/EDTA	Gibco® Life Technologies, Carlsbad, CA
2x Laemmli Sample Buffer	Bio-Rad Laboratories, Inc., Hercules, CA, USA
3-[4,5-dimethyl-thiazol-2-yl]-2,5-diphenyl tetrazolium bromide (MTT)	Invitrogen Life Technologies, Carlsbad, CA, USA
4',6-diamidino-2-phenylindole (DAPI)	Vector Laboratories, Burlingame, USA
5-bromo-2-deoxyuridine (BrdU),	Calbiochem, Darmstadt, Germany
Acrylamide/Bis solution (37.5:1)	Bio-Rad Laboratories, Inc., Hercules, CA, USA
Agarose (ultra pure)	Bio-Rad Laboratories, Inc., Hercules, CA, USA
AlamarBlue	Invitrogen Life Technologies, Carlsbad, CA, USA
Ammonium persulfate (APS)	Sigma Chemical Company, St Louis, MO, USA
Ampicillin	Sigma Chemical Company, St Louis, MO, USA
Anti-mouse CD31 (550274, BD)	BD Biosciences, Franklin lakes, NJ, USA
Anti-mouse IgG (BA-9200)	Vector Laboratories, Inc. Burlingame, CA, USA
Anti-mouse IgG, HRP-linked Antibody (Cat no. #7076)	Cell Signaling Technology Inc., Beverly, Massachusetts, USA
anti-rabbit IgG (BA-100)	Vector Laboratories, Inc. Burlingame, CA, USA

Anti-rabbit IgG, HRP-linked Antibody (Cat no. #7074)	Cell Signaling Technology Inc., Beverly, Massachusetts, USA
Anti- β -actin mouse monoclonal antibody (Cat no.C4: sc-47778)	Santa Cruz Biotechnology, Inc., Texas, USA
Bacto tryptone	BD Biosciences, Franklin lakes, NJ, USA
Bacto Yeast extract	BD Biosciences, Franklin lakes, NJ, USA
Blue/Orange Loading Dye, 6x	Promega Corporation, Madison, WI, USA
Boric acid	Sigma Chemical Company, St Louis, MO, USA
Bovine immunoglobulin	Bio-Rad Laboratories, Inc., Hercules, CA, USA
Bovine serum albumin (BSA)	Sigma Chemical Company, St Louis, MO, USA
Bradford reagent	Bio-Rad laboratories, Inc., Hercules, CA, USA
Bromophenol Blue	Sigma Chemical Company, St Louis, MO, USA
Chloroform	Merck Group, Darmstadt, Germany
Protease inhibitor Cocktails	Roche Diagnostics GmbH, Mannheim, Germany
DC protein assay reagents	Bio-Rad laboratories, Inc., Hercules, CA, USA
DH5 α TM strain of <i>Escherichia coli</i> (<i>E. coli</i>)	Invitrogen Life Technologies, Carlsband, CA, USA
Diethylpyrocarbonate	Sigma Chemical Company, St Louis, MO, USA
Dimethyl-sulphoxide (DMSO)	MP Biomedicals, CA, USA
Disodium Phosphate	Sigma Chemical Company, St Louis, MO, USA
Dithiothreitol (DTT)	Sigma Chemical Company, St Louis, MO, USA
Dual-Luciferase [®] Reporter (DLR TM) Assay System	Promega Co., Madison, WI, USA
Endothelial cell basal medium supplemented with Bullet Kit (EBM TM -2 SingleQuots)	Clonetics, Walkersville, MD
Ethanol (absolute, analytical grade)	Merck Group, Darmstadt, Germany
Ethidium bromide	Sigma Chemical Company, St Louis, MO, USA
Ethylenediaminetetraacetic acid (EDTA)	Sigma Chemical Company, St Louis, MO, USA
Fetal Bovine Serum (FBS)	Biowest Inc., Utah, USA

FuGENE 6 or FuGENE HD Transfection reagents	Promega Corporation, Madison, WI, USA
G418, Geneticin [®]	Sigma Chemical Company, St Louis, MO, USA
GelRed [™]	Biotium, Hayward, CA
Glycerol	Sigma Chemical Company, St Louis, MO, USA
Glycine	Bio-Rad laboratories, Inc., Hercules, CA, USA
Growth factor reduced Matrigel	BD Biosciences, Franklin lakes, NJ, USA
Hoechst 33258	Sigma Chemical Company, St Louis, MO, USA
Human IL-8 ELISA kit (ELISA MAX [™] Deluxe Sets)	Biolegend, San Diego, CA
Hydrochloric acid	Sigma Chemical Company, St Louis, MO, USA
Hydrogen peroxide	Sigma Chemical Company, St Louis, MO, USA
Hygromycin B	Gibco [®] Life Technologies, Carlsbad, CA
Isopropanol	Merck Group, Darmstadt, Germany
L-glutamine	Gibco [®] Life Technologies, Carlsbad, CA
Lipofectamine [®] RNAiMAX	Invitrogen Life Technologies, Carlsbad, CA, USA
Magnesium Chloride	Sigma Chemical Company, St Louis, MO, USA
Mercaptoethanol	Sigma Chemical Company, St Louis, MO, USA
Methanol	Merck Group, Darmstadt, Germany
Mouse anti-BrdU	Roche Applied Science, Germany
MTT (3-(4,5-Dimethylthiazol-2-yl)-2,5-Diphenyltetrazolium Bromide)	Invitrogen Life Technologies, Carlsbad, CA, USA
N-lauryl sarcosine (Sarkosyl)	Sigma Chemical Company, St Louis, MO, USA
Paraformaldehyde	Sigma Chemical Company, St Louis, MO, USA
Penicillin (1000U/ml)	Gibco [®] Life Technologies, Carlsbad, CA
Phosphatase Inhibitor Cocktail	Sigma Chemical Company, St Louis, MO, USA
Platinum [®] PCR SuperMix High Fidelity	Invitrogen Life Technologies, Carlsbad, CA, USA
Podoplanin (ab11936, Abcam)	Abcam, Cambridge, United Kingdom

Potassium phosphate	Sigma Chemical Company, St Louis, MO, USA
Prestained protein ladder, ExtraPro Broad Range (10-245 kDa)	1st BASE Pte Ltd, Singapore
PureLink™ HiPure plasmid purification kit	Invitrogen Life Technologies, Carlsband, CA, USA
PVDF membrane	Bio-Rad laboratories, Inc., Hercules, CA, USA
Restriction enzymes and CutSmart™ Buffer	New England BioLabs®, MA, USA
RNeasy® Mini Kit	Qiagen, Limburg, Netherlands
RPMI 1640 medium	Nacalai Tesque, Inc., kyoto, Japan
SIGMAFAST™ 3,3'-Diaminobenzidine tablets	Sigma Chemical Company, St Louis, MO, USA
Sodium chloride	Sigma Chemical Company, St Louis, MO, USA
Sodium dodecyl sulfate (SDS)	Sigma Chemical Company, St Louis, MO, USA
Sodium hydroxide	Sigma Chemical Company, St Louis, MO, USA
Sodium Phosphate	Sigma Chemical Company, St Louis, MO, USA
Sodium Tetraborate	Sigma Chemical Company, St Louis, MO, USA
Streptomycin (1000 µg/mL)	Gibco® Life Technologies, Carlsbad, CA
SuperScript® III One-Step RT-PCR System with Platinum® Taq DNA Polymerase	Invitrogen Life Technologies, Carlsband, CA, USA
SuperScript® VILO™ cDNA Synthesis Kit	Invitrogen Life Technologies, Carlsbad, CA, USA
SuperSignal West Pico Chemiluminescent Substrate kit	Pierce Biotechnology, Inc., Rockford, Illinois, USA
SYBR® GreenER™ qPCR SuperMix for ABI PRISM® (Invitrogen, CA)	Invitrogen Life Technologies, Carlsband, CA, USA
T4 DNA ligase	Roche Diagnostics GmbH, Mannheim, Germany
Tetramethylethylenediamine (TEMED)	MP Biomedicals, CA, USA
Tris(hydroxymethyl) aminomethane (Tris)	Sigma Chemical Company, St Louis, MO, USA
Triton X-100	Sigma Chemical Company, St Louis, MO, USA

TRIzol reagent	Invitrogen Life Technologies, Carlsband, CA, USA
Trypan Blue	Gibco [®] Life Technologies, Carlsbad, CA
Tween-20	Sigma Chemical Company, St Louis, MO, USA
Vectashield Elite ABC kit standard (PK-6100)	Vector Laboratories, Inc. Burlingame, CA, USA
Vectastain [®] Elite ABC Kit	In Vitro technologies, NZ
Wizard [®] SV Gel and PCR Clean-Up System	Promega Corporation, Madison, WI, USA
X-ray film	Konica Minolta Inc., Tokyo, Japan

2.2 Methods

2.2.1 Human cell lines

The human mammary carcinoma cell lines, T47D and MCF-7 were obtained from the American Type Culture Collection (Manassas, VA, USA). These cell lines were cultured in RPMI 1640 media (Nacalai Tesque, Kyoto, Japan) supplemented with 100 µg/mL streptomycin, 100 IU/mL penicillin, 10% heat-inactivated fetal bovine serum, and 2 mM L-glutamine at 37°C in a humidified 5% CO₂ incubator (Thermo Scientific, Waltham, MA). Human umbilical vein endothelial cells (HUVEC) (Clonetics Solingen, Germany) were a generous gift from Dr. Lim Yoon Pin, (Department of Biochemistry, National University of Singapore). HUVEC were cultured on a culture flask coated with 0.1% gelatin and were grown in endothelial cell basal medium (Clonetics, Walkersville, MD) supplemented with Bullet Kit (EBMTM-2 SingleQuots), 10% heat-inactivated fetal bovine serum, 100 IU/ml penicillin, and 100 µg/mL streptomycin at 37°C in a humidified 5% CO₂ incubator. HUVEC cultured from 4 - 8 passages were used for the experiments. Generation of MCF-7 and T47D cells with forced expression of TFF3 or depletion of TFF3 by siRNA have been previously described (Kannan *et al.*, 2010). The characteristics of the human mammary carcinoma cell lines and HUVEC are described in Table 2.

Table 2: Human cell lines description

Cell lines	Description
MCF-7	Mammary carcinoma cell line derived from a pleural effusion of an infiltrating ductal carcinoma (Dickson <i>et al.</i> , 1986). This cell line is well differentiated, epithelial, ER positive and non-invasive.
T47D	The T47D cell line is a ER+ mammary carcinoma cell line. It was isolated by Keydar <i>et al.</i> (1979) from a pleural effusion from a 54 year old female patient with an infiltrating ductal carcinoma of the breast. This differentiated epithelial substrain comprised cytoplasmic junctions and receptors for estrogen, other steroids and calcitonin.
HUVEC	Clonetics® Umbilical Vein Endothelial Cell (HUVEC) are tested positive for CD105 and CD31 endothelial markers, acetylated LDL uptake, von Willebrand factor VIII related antigen. It tested negative for alpha smooth muscle actin marker at passage four. HUVEC assayed for angiogenesis and vascular cell health markers.

2.2.2 Growth of human cell lines

The human cell lines were maintained using ATCC recommended conditions. Penicillin and streptomycin were also added to the media to prevent bacterial infection. Cells were grown in Greiner tissue culture treated flasks or plates at 37°C in humidity 5% CO₂ incubator. All tissue culture work was undertaken in a laminar flow hood with sterile conditions.

2.2.3 Passaging and harvesting of human cell lines

All cell lines were grown in 75 cm² culture flasks containing approximately 20 mL of recommended growth media until cells were 85 - 95% confluent, after which a portion was passaged into a new flask to allow continuation of stock cultures. The confluent cells were then passaged by removing the media and subsequently rinsing the cells twice with PBS. A sufficient volume of 1x trypsin/EDTA (approximately 1 mL) to cover the surface of the cells

was added and the flask incubated at 37°C in a humidified 5% CO₂ for two to five minutes. Cells were checked under the microscope to ensure that the cells had detached from the flask and most of them are individual cells. Following trypsinization, 5 - 8 mL of serum supplemented media was added to flask to neutralize the trypsin and the surface rinsed using a serological pipette. The cell suspensions were subsequently transferred to a 15 mL sterile Falcon tube and centrifuged at 1000 rpm for 5 min. The supernatant was discarded and cells pellet were resuspended in 10 mL of fresh serum-supplemented media. For maintaining of stock cultures, an appropriate cell number was seeded into a fresh culture flask and approximately 15 - 20 mL fresh media added, after which the cells were cultured at 37°C in a humidified 5% CO₂ incubator. For cell counting, 20 µL of the cells suspension (total volume 10 mL media) was transferred to an Eppendorf tube and mixed with 20 µL of trypan blue dye (0.4%). Cell counts were then carried out using a haemocytometer. The number of cells contained in four quadrants of 16 squares was counted (twice). The counted squares were sum up and averaged, upon which the resulting number was used to determine the amount of cells/mL using the following formula:

$$\text{Concentration of cells (cells /mL)} = (\text{Cells per 4 quadrants}/4) \times 10,000 \times \text{dilution factor}$$

$$\text{Total number of cells} = \text{Cells/mL} \times \text{final volume}$$

2.2.4 Storage of cell lines

Cells were trypsinized and resuspended in 10 mL media, counted and then centrifuged. Following removal of the supernatant, cells were resuspended in approximately 3 mL of ice cold freezing media. Aliquots of the cells suspension (1 mL) were transferred into cryogenic vial (Nalgene, Rochester, NY, USA). All vials were placed into an isopropanol containing freezing chamber (Nalgene, Rochester, NY, USA) and kept in a -80°C freezer for 24 hours to allow gradual cooling and freezing for cells preservation. The frozen cells were stored in the vapor phase of liquid nitrogen for long-term storage.

2.2.5 Revival of cell lines from liquid nitrogen storage

Cell aliquots from each cryogenic vial were thawed immediately in 10 mL of 37°C serum supplemented culture media and centrifuged at 1000 rpm for 5 min. The cells pellet was resuspended in 10 mL fresh serum supplemented culture media, transferred into a 25 cm² tissue culture flask, and cultured at 37°C incubator in humidified 5%CO₂. Media was changed the next day and every two days to allow growth of revived cells.

2.2.6 Transfection of mammalian cells

Transfection of specific DNA vectors was performed using FuGENE 6 (Promega, Madison, WI) as recommended by manufacture's instruction. Stable transfection required the additional selection of transfectants with appropriate antibiotics.

(i) Transient transfection:

Cells were plated at density of 400,000 cells per six-well plates one day before performing the transfection. When the cells reached 70 - 80% confluent, transient transfection was carried out to increase the transfection efficiency. For generation of mammary carcinoma cells with depletion of TFF3, mammary carcinoma cells were transiently transfected with a pSilencer 2.1-U6 hygro (Ambion, Austin, TX) expression vector that containing human TFF3 siRNA (Target DNA sequence: AAACAACGGTGCATAAATGAG) or control siRNA that encoding a siRNA comprises non-significant sequence similarity to human gene sequences. The expression vectors was constructed as previously described (Kannan *et al.*, 2010).

FuGENE 6 transient transfection was performed according to manufacturer's instruction. To prepare transfection solution required for 6-well plate, 12 µL of FuGENE 6 was diluted in 200 µL with serum free culture media and incubated for 10 minutes at room temperature. After that, 4 µg plasmid DNA was added into the diluted transfection reagent (FuGENE 6 reagent and plasmid DNA in serum free culture media at a 3:1 ratio). The FuGENE 6/DNA complex was incubated at room temperature for 20 minutes. The culture media was removed from cells and 1 mL of serum-free media was added to each well. The

FuGENE 6/DNA complex solution was added directly to the cells drop-wise. Following three to four hours incubation at 37°C, 500 µL of complete media was applied to each well. The transfected cells were cultured at 37°C in humidified 5% CO₂ incubator for 24 hours or 48 hours prior performing any assays.

(ii) Stable transfection:

For stable transfection, cells were cultured to 70 - 80% confluence in a 75 cm² culture flask and stably transfected with FuGENE 6 (Promega, Madison, WI) according to the manufacturer's instructions. For generation of the stable cell line expressing TFF3, the MCF-7 or T47D cells were stably transfected with an pIRESneo3 expression vector containing the TFF3 cDNA (designated as MCF7-TFF3 or T47D-TFF3) or an empty pIRESneo3 vector as a control (designated as MCF7-Vec or T47D-TFF3). Pooled stable transfectants were selected with RPMI media, containing 800 µg/mL G418 for 21-28 days. Depending on the cell lines utilized, pooled stable transfectants were selected in varying concentration of Geneticin (G418). Initially when cell death was maximal, the media was changed every two days. Following that media was changed every three-four days. After three-four weeks, cells were trypsinized and transferred into a new 25 cm² culture flask. Stable expression was confirmed by semi-quantitative RT-PCR and Western blot analysis. Cell lines were then expanded and 10 vials of each cell lines were frozen. Cells were maintained in culture for a maximum of four months, following which a new vial was revived to avoid clonal selection.

2.3 Co-culture assays

In order to determine the functional effects of TFF3 secreted from mammary carcinoma on endothelial cells, an indirect co-culture transwell system was employed, in which mammary carcinoma cells were plated into the membrane of transwell insert (0.4 µm pore size polyester transwell insert) (Corning, NY, USA) co-cultured with HUVEC seeded in the bottom well of companion plate. Mammary carcinoma cells with forced expression of TFF3 or depletion of TFF3 co-cultured with HUVEC to determine the stimulatory effects of

TFF3 on HUVEC monolayer proliferation, cell cycle progression, survival, and tubule formation *in vitro*. To determine the effects of TFF3 secreted from mammary carcinoma cells on HUVEC migration and invasion, modified Boyden migration/invasion chamber assays using 8 μ m transwell inserts (Greiner Bio-One GmbH, Germany) were conducted. Whereby, HUVEC were plated into the membrane of transwell insert co-cultured with mammary carcinoma cells seeded in the bottom well of companion plate.

2.3.1 RNAi transfection

The On-Target anti-IL-8 siRNA and control siRNA (non-targeted, random sequence) were purchased from Dharmacon (Chicago, IL) (Table 3). The Smartpool On-Targetplus Human IL-8 siRNA was a mixture of 4 SMART selection designed siRNA species targeting human IL-8 gene. Smartpool On-Target siRNAs designed to hybridize and destroy human IL-8 mRNA (Gen Bank Accession No. NM_000584). Subsequently, it silenced the human IL-8 gene or protein expression. The sequences of these Smartpool siRNAs were verified to be specific to human IL-8, thus eliminating the off-target effects. On-Targetplus non-targeting pool was a negative control siRNA with at least 4 mismatches to any rat, mouse, and human gene and microarray tested. The Smartpool On-Target siRNA and negative control were transfected into human mammary carcinoma cells using Lipofectamine® RNAiMAX Reagent (Invitrogen®, Carlsbad, CA, USA) according to manufacturer's instruction with slight modification. Briefly, mammary carcinoma cells were plated to be 70 - 80% confluent on a 6 well plate (400,000 cells/well) in complete media and incubated at 37°C for 24 hours prior transfection. Final concentration of siRNA and negative control was 20 nM as recommended. 4 μ L of Lipofectamine® RNAiMAX Reagent was diluted in 200 μ L serum-free media. Similarly, 2 μ L of siRNA and negative control was diluted in 200 μ L serum-free media. Gently mixed the contents of each tube by pipetting carefully up and down and incubated at room temperature for 5 minutes. The diluted siRNA or negative control was added to respective tubes containing diluted Lipofectamine® RNAiMAX Reagent (1:1 ratio). Gently

mixed the contents of each tube by pipetting carefully up and down and incubated at room temperature for 20 minutes. The culture media was removed from cells and 1 mL of serum-free media was added to each well. The siRNA-lipid complex solution was then added directly to the cells drop-wise. Following three to four hours incubation at 37°C, 500 µL of complete media was applied to each well. The transfected cells were cultured at 37°C in humidified 5% CO₂ incubator for 24 hours or 48 hours prior performing assays. The silencing of IL-8 gene mRNA expression after 24 hours transfection was measured by semi-quantitative RT-PCR to identify the efficiency of siRNA. Additionally, conditioned medium from the cells were collected after 48 - 72 hours transfection and the silencing of IL-8 protein expression was measured by Human IL-8 ELISA kit (ELISA MAXTM Deluxe Sets, Biolegend, San Diego, CA).

Table 3: The gene sequence of validated siRNAs and negative control

Smartpool On-Targetplus Human IL-8 siRNA, 10 nmol	Target sequence
On-Targetplus Smartpool siRNA J-004756-05, IL-8	GCAUAAAGACAUACUCCAA
On-Targetplus Smartpool siRNA J-004756-06, IL-8	GGACCACACUGCGCCCAACA
On-Targetplus Smartpool siRNA J-004756-07, IL-8	GCCAAGGAGUGCUAAAGAA
On-Targetplus Smartpool siRNA J-004756-08, IL-8	UGAAGAGGGCUGAGAAUUC
On-Targetplus Non-targeting pool, 5 nmol	

Source: Product datasheet from ThermoScientificBio.com/resource-library

2.3.2 Monolayer cell proliferation (Total cell number)

Mammary carcinoma cells with forced or depletion of TFF3 were trypsinized and seeded into six-well cell culture plates at a density of 50,000 cells/well. Cells were cultured in complete media for 24 hours at 37°C in 5% CO₂ incubator to ensure that they attached to the culture surface. Cell culture media was then changed into either 0.2% FBS or 10% FBS supplemented media. Assays were set up in triplicate and cells were counted every 24 hours

over two or three day periods. For HUVEC with forced or depleted expression of TFF3, counts were conducted over two or three days periods both for 0.2% FBS EBM or 10% FBS supplemented EBM medium, respectively. For co-culture assays, mammary carcinoma cells with forced or depleted expression of TFF3 (80,000 cells per transwell insert) were plated into the membrane of transwell insert (0.4 µm membrane pore size) (Corning Inc, NY, USA) in 10% FBS RPMI and incubated at 37°C for 24 hours after which the media was replaced with serum-free medium. HUVEC at density of 50,000 cells in serum-free EBM were seeded in bottom well of the companion plate. Assays were carried out for two to three days. Cells in each well were trypsinized with 0.5% trypsin and collected in 15 mL Falcon tubes. Cells were centrifuged at 1,000 rpm for 5 minutes to discard the supernatant and cell pellets was collected. Cells were then resuspended in 1 mL of supplemented media and counted using a haemocytometer.

2.3.3 5-bromo-2-deoxyuridine (BrdU) assay

Entry into S-phase of the cell cycle was determined by measuring the incorporation of 5-bromo-2-deoxyuridine (BrdU) (Kaulsay *et al.*, 2001). BrdU labeling cells were trypsinized and seeded in triplicate into 24-well cell culture plates at a density of 200,000 – 250,000 cells per well. Cells were incubated overnight at 37°C in 5% CO₂ incubator, and after 12 hours the media was removed and the cells washed 3 times with PBS. Cells were then incubated in serum-free media for 18 - 20 hours. Co-culture experiments were performed as described for the total cell number assay. After 18 - 20 hours incubation at 37°C in 5% CO₂, the cells were pulse labeled with 20 µM BrdU (10 µL of 10 mM BrdU in 5 mL of media) was for 30 minutes at 37°C in 5% CO₂. The media was discard and cells were washed 3 times with PBS. The procedure for detection of BrdU labeled cells is as below:

(i) Fixing

Cells were fixed by 4% formaldehyde diluted in PBS for 30 minutes at 4°C and were washed 3 times with PBS. The endogenous peroxidase in the cells was blocked by 3% H₂O₂

in methanol. 1 mL of freshly prepared 3% H₂O₂ was added to each well and plates were incubated on a rocker at room temperature for 30 minutes. At the end of incubation, H₂O₂ was removed and wells were washed 3 times with PBS for 5 minutes each wash. Cells were then incubated with 2N HCl (1 mL per well) on a rocker at room temperature for 1 hour. After removing HCl, cells were washed 2 times with 0.1 M borate solution followed by a 5 minutes PBS wash.

(ii) Blocking and incubation with antibodies

Cells were incubated with 1 mL blocking solution (2% horse serum in PBS) per well for 1 hour at room temperature on a rocker and then washed 3 times with PBS for 5 minutes each wash. 1 mL of primary antibody at 1:100 dilution (mouse anti-BrdU antibody, Roche Applied Science, Germany) was added into the cells and incubated overnight at 4°C. The Vectastain® Elite® ABC Kit (Vector Laboratories, Inc. Burlingame, CA, USA) was used in the following steps that included 2 hours incubation with 1 mL per well of secondary antibody solution at room temperature and 1 hour incubation with 1 mL per well of tertiary antibody solution at room temperature. All these incubations with different antibodies were performed with gentle agitation followed by 3 x 15 minutes washes with PBS.

(iii) Staining

The substrate solution was prepared by dissolving FAST 3,3-Diaminobenzidine hydrochloride (DAB) tablets (Sigma-Aldrich, MO, USA) in MilliQ water. 400 µL was added to each well and color development monitored. Staining was stopped with a PBS wash. Finally, cells were fixed in 70% cold ethanol at 4°C for 30 minutes, washed twice with PBS, and stored at 4°C until counted.

(iv) Determination of the BrdU labeling index

A total population of over 1000 cells was analyzed in ten arbitrarily chosen microscopic fields. Results were expressed as the percentage of cells synthesizing DNA (BrdU labeling index). Stained cells were counted using an OLYMPUS® IX71 Inverted Laboratory System Microscope, Olympus Optical Co., Tokyo, Japan.

2.3.4 Apoptosis assay

Bisbenzimidides are cell-permeable, A-T specific dyes, which can intercalate in the minor groove of A-T regions thereby fluorescently labeling DNA. In this assay, one member of the bisbenzimidides, Hoechst 33258, was employed. Apoptotic cell death was determined by fluorescent microscopic analysis of DNA staining patterns with Hoechst. Cells were plated at a density of 200,000 - 250,000 cells per well. After an overnight incubation at 37°C in 5% CO₂ in complete growth media to allow cells to attach, cells were treated with stimulation media (serum or serum-free; with or without drug treatment). Co-culture experiments were set up as described for the total cell number assay. After a culture period of 24 hours in serum-free media, media was carefully removed and the cells were fixed in 4% formaldehyde in PBS at 4°C for 30 minutes. The cells were subsequently stained the karyophilic dye Hoechst 33258 (4 µg/mL Hoechst 33258, 1% Triton X-100 in PBS) at room temperature in the dark for 30 minutes. The staining solution was removed, washed twice with PBS, and culture plate was stored at 4°C. Apoptotic nuclear morphology was determined and examined under an inverted UV fluorescence microscope (Olympus). As compared to viable cells, the nuclear morphology of apoptotic cells characterized with nuclear fragmentation and condensation as well as the higher intensity of blue fluorescence of the nuclei. For statistical analysis, over 1,000 cells were counted in ten random microscopic fields at 200x magnification.

2.3.5 Invasion and migration assays

Migration and invasion assays were performed using modified Boyden chamber consisting cell culture transwell inserts (8 µm pores, Greiner Bio-One, Germany) and companion plates (24-well format) according to the manufacturer's instructions. For invasion assays, inserts were coated with growth factor reduced Matrigel (BD Bioscience) before plating the cells. Matrigel was diluted in serum-free media at 1/10 for MCF-7 and 1/50 for HUVEC respectively. HUVEC (30,000 cells) or mammary carcinoma cells with forced or

depleted expression of TFF3 (50,000 cells) in serum-free media was seeded into the membrane of transwell inserts and complete media was added to the bottom well of the companion plate. For co-culture assays, mammary carcinoma cells with forced or depleted expression of TFF3 (250,000 cells) in 10% FBS RPMI media were plated in the bottom well of the companion plate and incubated at 37°C for 24 hours after which the media was replaced with serum-free media. A total of 30,000 HUVEC in serum-free EBM media were seeded into the membrane of transwell inserts. For migration and invasion assays using anti-IL-8 monoclonal antibody, mammary carcinoma cells with forced or depleted expression of TFF3 (250,000 cells) plated in 10% FBS RPMI media were plated in the bottom well of the companion and incubated at 37°C for 24 hours after which the media was replaced with serum-free medium containing anti-IL-8 monoclonal antibody (50 µg/mL) and IgG control. A total of 30,000 HUVEC in serum-free media were seeded into the membrane of transwell inserts. For assays using exogenous human recombinant TFF3 (rhTFF3), different dilution of rhTFF3 in serum-free media and Bovine serum albumin (BSA) used as control were added to the bottom well of the companion plate. After 24 hours incubation at 37°C, cells that had migrated or invaded to the lower surface of the transwell inserts were washed twice with PBS, fixed with 4% paraformaldehyde for 20 minutes, and stained with Hoechst 33258 (4 µg/mL Hoechst 33258, 1% Triton X-100 in PBS) at room temperature in the dark for 30 minutes. The staining solution was then discarded, washed twice with PBS, and culture plate was stored at 4°C. The cells migrated to the lower surface of the entire transwell inserts were counted (OLYMPUS® IX71 Inverted Laboratory System Microscope, Olympus Optical Co., Tokyo, Japan).

2.3.6 Tubule formation *in vitro*

Growth factor reduced Matrigel (BD Bioscience) was thawed overnight in the fridge. The thawed Matrigel spread evenly over each well (300 µL) of a 24-well plate. The plates were incubated at 37°C for 30 minutes in a cell culture incubator to allow the Matrigel to

solidify. A total of 30,000 HUVEC (30,000 cells/well for 24-well plate) in serum-free media were seeded in the Matrigel, incubated at 37°C for 12 hours, and fixed with 4% paraformaldehyde at room temperature for 20 minutes. Tubules were visualized under the microscope at low magnification (x40). For co-culture experiments, mammary carcinoma cells with forced or depleted expression of TFF3 were plated at 50,000 cells per transwell inserts (0.4 µm pores) (Corning Inc, NY, USA) in 10% FBS for 24 hours after which the media was replaced with serum-free media. The mammary carcinoma cells plated into the transwell inserts co-cultured with HUVEC seeded in the Matrigel. The plate was incubated at 37°C for 12 hours and tubules were visualized under the microscope at low magnification (x40). For data analysis, tubules formed by HUVEC in Matrigel of the entire transwell insert was photographed and analyzed by using ImageJ software (version 2.02; University of Texas Health Scientific Center at San Francisco).

2.3.7 Luciferase reporter assay

(i) Plasmids

Several plasmids such as pGL3-basic vector, pGL-IL-8-152 reporters were generous gifts from Prof. Takashi Tokino (Department of Molecular Biology, Cancer Research Institute, Sapporo Medical University, Sapporo, Japan). The pGL3-basic vector was used as control plasmid. Fragment containing 5' flanking regions of the IL-8 gene were subcloned upstream of a luciferase reporter gene. pGL-IL8-152 reporter construct encompassing nucleotides -152 to +44 of the IL-8 promoter, which containing transcription factors, AP-1, NF-IL-6 and NFκB binding sites. The TATA box, and the NF-IL-6, NFκB and AP-1 binding sites are located at -13, -70, -80 and -120, respectively. Human IL-8 promoter reporter vector (full length, -4800 to + 104 bp) was a generous gift from Dr. Suswam A. Esther (Department of Neurology, University of Alabama in Birmingham, USA), and pRL-CMV control reporter vector (Promega, Madison, WI, USA) was used as an internal control for transfection efficiency of

luciferase reporter assay. The pcDNA 3.1 empty vector and pcDNA 3.1 expression vector containing human STAT3 siRNA have been previously described (Mohankumar *et al.*, 2008).

(ii) Luciferase reporter assay

Cells with forced or depleted expression of TFF3 were plated at a density of 200,000 cells per well in 12-well plate in triplicates and cultured in RPMI medium supplemented with 10% FBS at 37°C for 24 hours before transfection. Luciferase reporter assay was performed as previously described (Fan and Wood, 2007). Briefly, cells with forced expression of TFF3 or depletion of TFF3 transiently transfected with 2 µg of a reporter plasmids including human IL-8 promoter reporter vector (-4800 to + 104 bp) or pGL-IL8-152 reporter (-152 to +44 bp) and 40 ng pRL-CMV control reporter vector (Promega, Madison, WI, USA) using FuGENE 6 reagent according to the manufacturer's instructions. *Renilla* luciferase reporter vector used as control for transfection efficiency. For determination of IL-8 promoter activity in MCF7-Vec and MCF7-TFF3 with depletion of STAT3, MCF-7 cells with forced expression of TFF3 transiently transfected with 1 µg pcDNA3.1 empty vector containing control siRNA or pcDNA3.1 expression vector containing STAT3 siRNA, 1 µg human IL-8 promoter reporter (-4800 to + 104 bp), and 40 ng pRL-CMV control reporter vector (Promega, Madison, WI, USA) using FuGENE 6 reagent.

After 24 hours transient transfection, the reporter activities were measured by luciferase reporter assay using Dual-Luciferase® Reporter (DLR™) Assay System (Promega, Madison, WI, USA). *Renilla* luciferase activity was used as an internal control. Briefly, 250 µL of 1x Passive Lysis Buffer (PLB) was added to each well of 12-well plate. Cells were incubated with PLB for 15 minutes on shaker and the cell lysate was then transferred to Eppendorf tubes. The cell lysate (20 µL) was added to each well of a white 96-well microtiter plate (Greiner Bio-One, Frickenhausen, Germany). Luciferase Assay Buffer (50 µL) was dispensed into each well and mixed by tapping the plate gently. Firefly luciferase activity of the samples were measured by an Infinite 200 PRO micro plate reader (Tecan, Maennedorf, Switzerland), which was programmed to two sec measurement delay followed by a 10 second

measurement read for luciferase activity of samples. Subsequently, Stop & Glo[®] reagent (50 μ L) was immediately added to each well mixed by tapping the plate gently. The *Renilla* luciferase activity was measured for normalization of transfection efficiency.

2.4 Biochemistry and molecular biology methods

2.4.1 IL-8 ELISA

A human IL-8 ELISA kit (ELISA MAX[™] Deluxe Sets, Biolegend, San Diego, CA) was used to quantify the human IL-8 protein in conditioned medium of mammary carcinoma cells with forced expression of TFF3, depletion of TFF3, depletion of IL-8, and depletion of STAT3. Mammary carcinoma cells were grown to 70 - 80% confluence in a six-well plate. The cells were washed with PBS, pH 7.4 and the media was changed to serum-free for 24 hours. The media was collected after 24 hours and the ELISA assay was performed as per manufacturer's instructions. Briefly, the 96-well flat clear bottom of polystyrene microplate (Nunc[™], Thermo Scientific) was coated with 100 μ L diluted IL-8 specific monoclonal antibody and incubated overnight at 4°C. The plate washed 4 times with 300 μ L Wash Buffer (0.05% Tween-20 in PBS, pH 7.4) per well and the residual buffer was blotted by firmly tapping plate upside down on absorbance paper. The plate was then blocked with 200 μ L 1x Assay Diluent A to block non-specific binding and reduce background. The plate was then sealed with adhesive film and incubated for 1 hour at room temperature with shaking at 200 rpm on a plate shaker. While the plate is being blocked, the appropriate sample dilutions (1/100 dilution for conditioned media from HUVEC and conditioned media from mammary carcinoma cells can be used directly) and standards were prepared. A 1,000 μ L of top standard recombinant human IL-8 at 1,000 pg/mL was prepared from stock solution (5ng/ mL) in 1x Assay Diluent A. Six two-fold serial dilutions of the 1,000 pg/mL top standard with 1x Assay Diluent A in separate tubes. After diluting, the human IL-8 standard concentrations were 1,000 pg/mL, 500 pg/mL, 250 pg/mL, 125 pg/mL, 62.5 pg/mL, 31.3 pg/mL, and 15.6 pg/mL, respectively. 1x Assay Diluent A served as the zero standard (0 pg/mL). The plate

washed 4 times with 300 μ L Wash Buffer. A total of 100 μ L of standards and conditioned medium of samples were added to the appropriate wells. The plate was sealed with adhesive film and incubated at room temperature for 2 hours with shaking at 200 rpm on a plate shaker. The plate was then washed with 4 times with Wash Buffer. Biotinylated Detection Antibody diluted at 1:200 dilution in 1x Assay Diluent A was added into each well (100 μ L/well), sealed the plate, and incubated at room temperature for 30 minutes with shaking. The plate was washed 4 times with Wash Buffer. Avidin-HRP diluted at 1:1,000 in 1x Assay Diluent A was added to each well (100 μ L/well), sealed the plate, and incubated at room temperature for 30 minutes with shaking. The plate was then washed 5 times with Wash Buffer. For this final wash, soaked wells in Wash Buffer for 1 minute for each wash to minimize background noise. TMB Substrate Solution C was added into each well (100 μ L/well) and incubated in the dark for 15 minutes. Positive wells turned blue color. The reaction was stopped by adding 100 μ L of Stop Solution (2N H_2SO_4) to each well. Positive wells turned from blue to yellow. Absorbance reading was read at 450 nm within 30 minutes. The reference absorbance at 570 nm was subtracted from the absorbance at 450 nm. Results were expressed as concentration of IL-8 in the conditioned media (ng/mL).

2.4.2 RNA isolation

(i) RNA isolation using TRIzol reagent

Total RNA was extracted from exponentially growing cells (70% confluence) using TRIzol reagent. Cells were lysed by adding 1 mL TRIzol per 10 cm^2 culture flask. The homogenized sample was incubated at room temperature for 5 minutes. Next, 0.2 mL of chloroform per mL of TRIzol reagent was added to each tube and mixed vigorously for 15 seconds. After centrifugation at 12,000g for 15 minutes at 4°C, the aqueous phase (RNA) was pipette out to a fresh tube and precipitated by adding 0.5 mL of 100% isopropanol per mL of TRIzol and incubated at room temperature for 10 minutes. A second centrifugation (at 12,000g for 15 minutes, 4°C) was performed and the supernatant was discarded. The RNA

pellet was washed in 1 mL of 75% ethanol per mL TRIzol reagent used in the initial homogenization by centrifugation at 7,500 g for 5 minutes at 4°C to remove salt. A third centrifugation was then performed at 7,500 g for 5 minutes at 4°C and the pellet was air dried at room temperature and resuspended in RNase-free water or Diethylpyrocarbonate (DEPC) dH₂O. RNA sample was incubated in a water bath or heat block set at 55 - 60°C for 10-15 minutes to increase the solubility of the RNA. The RNA sample can be used for downstream application or stored at -80°C. The concentration and purity of RNA was determined spectrophotometrically using the ratios A260/A280 nm and A260/A230 nm. A ratio less than 1.8 may indicate the presence of contaminants within the sample.

(ii) RNA isolation using RNeasy[®] Mini Kit

Total RNA was isolated from exponentially growing cells (70% confluence) using RNeasy[®] Mini Kit (Qiagen, Limburg, Netherlands) as described by manufacturer's instruction. Briefly, cells were lysed by adding an appropriate volume of Buffer RLT containing either 1% β-mercaptoethanol or 2% 2M dithiothreitol (2M DTT), centrifuged at 12,000 rpm for 3 minutes, transferred the supernatant to a new microcentrifuge tube. Equal volume of 70% ethanol was added to the lysate (1:1 ratio), and mix well by pipetting. A total volume of 700 µL of the sample including any precipitate was transferred to an RNeasy Mini spin column placed in a 2 mL collection tube, centrifuged at 12,000 rpm for 1 minute, and flow-through was discarded. RNeasy spin column washed by adding 700 µL Buffer RW1, centrifuged at 12,000 rpm for 1 minute, and flow-through was discarded. After first washing, 500 µL Buffer RPE was added to the RNeasy spin column and centrifuged at 12,000 rpm for 1 minute. Addition of 500 µL Buffer RPE to the RNeasy spin column, centrifuged at 12,000 rpm for 2 minutes, and flow-through was discarded. The residual of buffer was removed out from the spin column by centrifuged at 12,000 rpm for 1 minute. The RNA sample was eluted by adding 30-50 µL RNase-free water directly to the spin column membrane and centrifuged at 12,000 rpm for 2 minutes. The concentration and purity of RNA was determined spectrophotometrically using the ratios A260/A280 nm and A260/A230 nm.

2.4.3 cDNA synthesis

Total RNA was converted to cDNA using SuperScript® VILO™ cDNA Synthesis Kit, which provides the high-temperature capability of SuperScript® III Reverse Transcriptase in an optimized conditions for generation of first-strand cDNA that commonly used in real-time quantitative RT-PCR (qPCR). For a single reaction, all components were combined in a tube on ice which included 5x VILO™ Reaction Mix (4 µL), 10x SuperScriptR Enzyme Mix (2 µL), RNA (up to 2.5 µg), DEPC-treated water to 20 µL reaction. The contents of the tube were gently mixed and reactions were incubated at 25°C for 10 minutes and followed by 42°C for 60 minutes. The reaction was terminated at 85°C for 5 minutes. 1 µL (2 U) of *E. coli* RNase H was added and the tube was incubated at 37°C for 20 minutes. The cDNA was stored at -20°C until use.

2.4.4 PCR

Amplification of DNA templates was carried out using Platinum® PCR SuperMix High Fidelity (Invitrogen). The PCR mixture contains 22 U/ml *Pyrococcus* species *GB-D* thermostable polymerase, complexed recombinant *Taq* DNA polymerase and Platinum®, *Taq* Antibody in PCR buffers. For a single reaction, all components were combined in a reaction tube on ice (Table 4).

Table 4: Reaction components for PCR

Component	Volume
Platinum® PCR SuperMix High Fidelity	10.0 µL
DNA template (1-2 µg)	2.0 µL
Sense primer (10 µM)	1.0 µL
Anti-sense primer (10 µM)	1.0 µL
Autoclave MiliQ water	6.0 µL
Total reaction volume	20.0 µL

RT-PCR reactions were performed on a Peltier PCR Thermal Cycler (PTC-100, MJ research, Ramsey, MN). A negative control, including every component similar to normal reaction except template RNA, was included in each experiment. Each reaction started with two-step amplification program of initial denaturation at 95°C for 10 minutes, followed by PCR thermal cycle. The PCR cycling consisted of three steps including denaturation at 94°C for 30 seconds, annealing at specified temperature for 60 seconds, and extension at 72°C for 1 minute for the indicated cycles. The specific annealing temperature, number of cycles, and the primer sequences for individual reaction are listed in Table 6. Amplified β -actin served as an internal control for RNA quantity and quality. Amplified reactions were separated on a 1.5% agarose gel prepared in Tris-Boric acid-EDTA buffer (TBE 1x) containing of 1x GelRed™ (Biotium, Hayward, CA) or 1% ethidium bromide solution.

2.4.5 Semi-quantitative RT-PCR

Semi-quantitative RT-PCR was performed by using Invitrogen™ OneStep RT-PCR System with Platinum® *Taq* DNA polymerase Kit (Invitrogen). A master mix was prepared according to the following protocol to avoid localized differences in salt concentration (Table 7). Invitrogen™ OneStep RT-PCR Enzyme Mix was the last component added into the master mix In order to keep the maximum enzyme activity. The reaction components in master mix were enlisted as following (Table 5):

Table 5: Reaction components for semi-quantitative RT-PCR

Component	Volume
2x Reaction Mix	12.5 μ L
Template RNA (0.01 pg - 1 μ g)	variable
Sense primer (10 μ M)	1 μ L
Anti-sense primer (10 μ M)	1 μ L
SuperScript® III RT/ Platinum® <i>Taq</i> Mix	2 μ L
Autoclave MiliQ water	top to 25 μ L

RT-PCR reactions were performed on Peltier PCR Thermal Cycler (PTC-100, MJ research, Ramsey, MN). A negative control, including every component similar to normal reaction except template RNA, was included in each experiment. Each reaction started with 30 minutes reverse transcription at 50°C followed by 15 minutes at 95°C. The PCR cycling consisted of three steps including denaturation at 94°C for 30 seconds, annealing at specified temperature for 30 seconds, and extension at 72°C for 2 minutes for the indicated cycles. The specific annealing temperature, number of cycles, and the primer sequences for individual reaction are listed in Table 6. Amplified β -actin used as an internal control for RNA quantity and quality. Amplified reactions were separated on a 2% agarose gel prepared in Tris-Boric acid-EDTA buffer (TBE 1x) containing of 1x GelRed™ (Biotium, Hayward, CA) or 1% ethidium bromide solution. When the gel was polymerized, it was placed onto the GT agarose gel electrophoresis system that filled with 1x TBE buffer. A defined amount of RT-PCR product (approximately 10-20 μ L) was mixed with 1.5 - 3.0 μ L 6x DNA loading dye and then loaded into each lane of the agarose gel. A 100 bp or 1 Kb plus DNA ladder was used as a base pair marker. Electrophoresis was performed at 80 - 100 V for 20 - 40 minutes. RT-PCR products were visualized under UV light, photographed, and analyzed.

Table 6: Primers and PCR parameters for RT-PCR analysis

Gene	Primer sequence (5'-->3')	Product size (bp)	Annealing Temperature (°C)	PCR cycles
<i>VEGF-A</i>	F: CATCACCATGCAGATTATGC R: AAAGTGCTCTGCGCAGAGTC	437 & 305	55	35
<i>VEGF-B</i>	F: GGATAGATGTGTATACTCGC R: TGTCTGGGTTGAGCTCTAAG	527 & 426	55	35
<i>VEGFR1</i>	F: GAGAGTATCACTCAGCGCAT R: GCAGTAAAATCCAAGTAACG	271	50	35
<i>VEGFR2</i>	F: TCCCGAGTTCTGGGCATTTC R: TGTACACGACTCCATGTTGG	451	50	35
<i>IL-8</i>	F: GAATGGGTTTGCTAGAATGTGATA R: CAGACTAGGGTTGCCAGATTAAAC	129	60	35
<i>CXCR1</i>	F: AGGGGCCACACCAACCTTCTG R: AGTGCCTGCCTCAATGTCTCCA	364	65	35
<i>CXCR2</i>	F: CAGTTACAGCTCTACCCTGCC R: CCAGGAGCAAGGACAGACCCC	451	65	35
<i>STAT3</i>	F: GATCCAGTCCGTGGAACCAT R: ATAGCCCATGATGATTTCAGCAA	75	60	35
<i>TFF3</i>	F: CTTGCTGTCTCCAGCTCT R: CCGGTTGTTGCACTCCTT	125	60	35
<i>β-ACTIN</i>	F: ATGATATCGCCGCGCTCG R: CGCTCGGTGAGGATCTTCA	581	62	30

2.4.6 Real-time quantitative PCR

Total RNA was isolated from mammary carcinoma cells with forced expression of TFF3. Total RNA was then converted to cDNA by using SuperScript® VILO™ cDNA Synthesis (Invitrogen, CA) as described in section 2.4.3. Real-time qPCR was performed using the SYBR® GreenER™ qPCR SuperMix for ABI PRISM® (Invitrogen, CA) following the manufacturer's protocol. The q-PCR experiment and data analysis were conducted by an ABI 7700® real-time PCR system (Applied Biosystems, USA). Multiple gene markers and three housekeeping genes (HKG) were utilized for real-time qPCR analysis. Real-time qPCR reaction mixture (20 µL) comprised of 12.5 µL SYBR® GreenER™ qPCR SuperMix, 2 µL of 200 nM primer (forward and reversed primers), and 3.5 µL RNase-free water was prepared. 5 ng of total cDNA (2 µL) was then added to the Real-time qPCR reaction mixture. Each

gene marker (Table 7) was added to a qPCR 384-well plate and run in triplicate. Real-time qPCR was performed using a two-step amplification program of initial denaturation at 95°C for 10 minutes, followed by 40 cycles of 95°C for 20 seconds, 60°C for 30 seconds and 70°C for 30 seconds. At the end of the amplification, a melting curve analysis consisted of denaturation at 95°C for 1 minute and re-annealing at 55°C for 1 minute was performed. Standard curves were constructed from each experimental plate using serial 5-fold dilutions of untreated cDNA. The Ct-value for each reaction was calculated in order to obtain their geometric mean. The equation $E = 10^{(-1/\text{slope})}$ was used to calculate the amplification efficiencies and ranged from 90 - 104% for all gene markers (Heid *et al.*, 1996). Melting curve analysis was used to ensure that there was no unspecific amplification or primer dimer in any of the reactions. Each experiment was carried out at least three times with independent samples. The gene expression of the gene marker was expressed as “fold change” and the gene expression of the gene marker in three repeated experiments were averaged (P value < 0.05 indicated statistically significant). Fold change > 2.0 indicated significant increased in mRNA level. The relative expression was calculated to compensate potential differences between markers, based on the efficiency (E), normalized by three housekeeping genes included β -actin, HPRT and GAPDH, and the Ct difference (Δ) of sample versus control ($\Delta C_{t, \text{sample-control}}$). Relative expression = $2^{-(C_{t, \text{Sample}} - C_{t, \text{HKG}}) - (C_{t, \text{Control}} - C_{t, \text{HKG}})}$; Relative expression = $2^{-\Delta\Delta C_t}$. Changes in relative gene expression > 2.0-fold were taken as significant.

Table 7: Oligonucleotide primers of angiogenic markers for real time qPCR

Gene	Primer sequence (5'-->3')
<i>VEGF-A</i>	F: TACCTCCACCATGCCAAG R: GGTACTCCTGGAAGATGTC
<i>IL-8</i>	F: GAATGGGTTTGCTAGAATGTGATA R: CAGACTAGGGTTGCCAGATTTAAC
<i>ANGPT1</i>	F: CTCGCTGCCATTCTGACTCAC R: GACAGT TGCCATCGTGTCTG
<i>ANGPT2</i>	F: TGGGATTTGGTAACCCCTTCA R: GTAAGCCTCATTCCTTCCC
<i>COL18A1</i>	F: TACCACTTCCCCAGCCTCTTCT R: TGCACC AGGTTCTGTGTAGAGC
<i>TNF</i>	F: CCAGGCAGTCAGATCATCTTCTC R: AGCTGGTTATCTCTCAGCTCCAC
<i>TEK</i>	F: GCTTGCTCCTTTCTGGAAGTGT R: CGCCACCCAGAGGCAAT
<i>TGFB1</i>	F: GCCCTGGACACCAACTATTG R: CGTGTCCAGGCTCCAAATG
<i>TGBS1</i>	F: CTGCTCCAATGCCACAGTTC R: GGAGCCCTCACATCGGTTG
<i>GADPH</i>	F: TGCACCACCAACTGCTTAGC R: GGCATGGACTGTGGTCATGAG
<i>HPRT</i>	F: TGACACTGGCAAAACAATGCA R: GGTCCTTTTCACCAGCAAGCT
<i>β-ACTIN</i>	F: TTCCTGGGCATGGAGTC R: CAGGTCTTTGCGGATGTC

2.5 Plasmid DNA amplification

2.5.1 Bacterial strains

The *Escherichia coli* (*E.Coli*) strain DH5 α TM was obtained from Invitrogen (Groningen, The Netherlands). The genotype is DH5 α : ϕ 80dlac Δ ZM15, Δ (lacZY A-argF)U169, deoR, recA1, endA1, hsdR17(r-k, mk+), phoA, supE44, thi-1, gyr A96, rel A1 λ .

2.5.2 Growth of bacterial cultures

All bacterial cultures were grown aerobically in either liquid Luria-Bertani (LB) or on solid LB/agar plates at 37°C. Depending on the specific experiments, as indicated in

appropriate sections, relevant antibiotics and additives were further added for selective growth.

2.5.3 Bacterial transformation of plasmids

Plasmids were amplified by transforming into a DH5 α TM strain of *Escherichia coli* (Invitrogen, Carlsbad, CA, USA). Heat-shock competent DH5 α TM bacteria were mixed with the plasmid and incubated on ice for 30 minutes. Transformation was performed using a heat shock method by placing the mixed bacteria and DNA in 42°C water bath (Grant Instruments Ltd., Cambridge, UK) for 2 minutes, immediately followed by cooling on ice for 5 minutes. LB Broth (1 mL) was added to each Eppendorf tube and incubated in the 37°C incubator (Sanyo Electric Co. Ltd., Japan) for 1 hour. Cultures were then spread on a LB agar plates. Due to the presence of a specific cassette present on the cloned plasmid (such as ampicillin in pIRES vector), transformed bacteria were resistant to the corresponding antibiotic and could be utilized as a selectable marker for positively transformed colonies. For instance, 100 μ g/mL ampicillin is employed in selection of bacteria transformed with the pIRES plasmid. After bacterial plates were incubated in the 37°C incubator for 20 hours, a single colony from each petri dish was picked and placed in 200 mL of LB Broth containing 100 μ g/mL ampicillin. Cultures were grown at 37°C with vigorous shaking (250 rpm) in a Bioline® automatic incubator shaker (Edwards Instrument Co., Narellan, NSW, Australia) for 20 hours.

2.5.4 Plasmid DNA purification

Bacterial transformation of plasmid DNA was initially performed by 20 hours incubation at 37°C with vigorous shaking in antibiotic-supplied LB broth. Next, extraction and purification of plasmid DNA from transformed DH5 α TM bacteria was carried out using a PureLinkTM HiPure plasmid purification kit (Invitrogen, CA). The bacterial cells were harvested by centrifugation at 4,000 rpm for 10 minutes at 4°C using a TOMY MX-300 high speed refrigerated centrifuge (TOMY SEIKO CO., LTD, Japan). The pellet was collected and

resuspended in 10 mL chilled Suspension Buffer S1 with RNase by vortexing until homogenous, followed by addition of 10 mL Lysis Buffer (B7) and mixing thoroughly by gently inverting the capped Falcon tube 4-6 times until the lysate mixture was thoroughly homogenous. After 5 minutes incubation at room temperature, 10 mL Precipitation Buffer (N3) was immediately mixed with the lysate by inverting the tube until the mixture was thoroughly homogeneous. The mixture was then centrifuged at 15,000g for 10 minutes at room temperature. During this period, 30 mL of Equilibration Buffer (EQ1) was applied to equilibrate the PureLink™ HiPure Maxi Column. The DNA containing supernatant was loaded onto the equilibrated PureLink™ HiPure Maxi Column and allowed the solution in the column to drain by gravity. Columns were washed with 60 mL Wash Buffer (W8) and allowed the solution in the column to drain by gravity. Subsequently, the plasmid DNA was eluted with 15 mL Elution Buffer (E4). Isopropanol (10.5 mL) was mixed with the eluate at room temperature and centrifuged at 15,000g for 30 minutes at 4°C to precipitate the DNA. The DNA pellet was washed with 5 mL of 70% ethanol at room temperature and then re-precipitated by centrifugation at 12,000 g for 10 minutes at 4°C. The supernatant was carefully decanted and the pellet allowed to air dry before being redissolved in a suitable volume (50 - 200 µL) of ultrapure water. The concentration and purity of DNA measured using NanoDrop® ND-1000 Spectrophotometer (Thermo Scientific) and determined spectrophotometrically by UV absorbance at 260 nm or ratios A260/A280 nm. The purified DNA was stored at -20°C.

Small-scale plasmid DNA preparation was carried out using a Qiagen Miniprep Kit (Qiagen, Germany) according to the manufacturer's instructions. The 5 mL overnight bacteria culture was harvested by centrifugation at 16,000g for 15 minutes. The cell pellet was resuspended in Resuspension Solution, followed by the addition of Lysis Solution (0.2 M NaOH and 1% SDS) and Neutralization Solution. The lysate was centrifuged at 16,000 rpm for 10 minutes at room temperature, and the supernatant was transferred to a spin column. After spin for one minute, the column was washed by Washing Solution diluted with 95%

ethanol (162.8 mM potassium acetate and 27.1 mM Tris-HCl, pH 7.5). The column was centrifuged at 16,000 rpm for 1 minutes. The plasmid DNA was eluted in 50 μ L ultrapure water.

2.5.5 DNA purification from agarose gel

DNA subjected to agarose gel electrophoresis, as described above, was visualized under UV light and the desired band excised with a sterile scalpel. The gel fragment was placed in a sterile Eppendorf tube and membrane binding solution from the Wizard[®] SV Gel and PCR Clean-Up System (Promega) was added (ratio of 10 μ L solution per 10 mg of agarose gel slice). The mixture was vortexed and incubated at 50-60°C until the gel was dissolved. DNA purification was processed by centrifugation. The gel mixture was transferred to the SV minicolumn and centrifuged for 1 minute at 16,000 g. The liquid was discarded and the column was washed 2 times for 25 minutes at 16,000 g. The SV column was carefully transferred to a clean microcentrifuge tube and 50 μ L of nuclease free water was added. The tube was then centrifuged for 1 minute at 16,000g and the microcentrifuge tube containing the eluted DNA was stored at -20°C.

2.6 Determination of protein expression

2.6.1 Protein extraction

Cells were plated in supplemented media at 60 - 70% confluence and incubated at 37°C for 24 hours. Cells were washed once with ice cold PBS and harvested by mechanical scraping. The cells were resuspended in RIPA buffer (50 mM Tris-HCL pH 7.4, 1% Nonidet P-40, 150 mM NaCl, 1 mM EDTA, 1 mM NaF, 1mM PMSF, 1 mM Na₃VO₄, 1x protease inhibitor) and incubated for 30 minutes on ice with vortexing every 5 minutes. From this step onwards, all procedures were performed on ice to avoid protein degradation. Lysates were centrifuged for 15 minutes at 16,000g and the supernatant collected. Lysis buffer (2% SDS, 20% glycerol, 60 mM Tris-HCl pH 6.8, 1x protease inhibitor) was used for proteins

containing a significant amount of disulfide bonds and subsequently harder to lyse. In this case, cells were washed three times with ice cold PBS for 10 minutes, dried and placed at -80°C for one hour. 200 µL of lysis buffer was added to the petri dish and cells were harvested by mechanical scraping. Cell lysate was collected into an individual pre-chilled Eppendorf tube and sonicated in an 80T SONICLEAN benchtop ultrasonic cleaner (Soniclean Pty. Ltd., SA, Australia) for 1 minute. Finally, centrifugation was performed at 16,000g for 15 minutes at 4°C. The supernatants were transferred to new Eppendorf tubes and stored at -80°C or use immediately in subsequent assays. The protein concentration was measured in triplicates using DC protein assay (Bio-Rad).

2.6.2 Conditioned medium for concentration of protein

Cells were seeded in a 6-well plate at density of 200,000 cells in supplemented media and incubated at 37°C for 24 hours or 48 hours. After which, media were changed to serum-free medium and incubated at 37°C for 24 hours. Conditioned medium from the cells were collected and stored at -80°C or proceed to ultrafiltration for concentration of protein using an Amicon® Ultra-0.5 centrifugal filter unit with a nominal molecular weight limit (NMWL) of 3 KDa (Milipore, Darmstadt, Germany). Sample recovery was 90% and molecular weight of the protein > 3 kDa retained by the membrane. Conditioned medium was loaded into the Amico® Ultra filter device and centrifuged at 14,000g for 15 minutes at 4°C. To recover the concentrated solute, Amico® Ultra filter device was placed upside down in a clean microcentrifuge tube and centrifuged at 1,000g for 2 minutes in order to transfer the concentrated sample from the device to the tube. The protein concentration in the conditioned medium was determined by Bradford Assay.

2.6.3 Bradford assay

Bradford assay was used to determine the total protein concentration of a sample. This method is based on the proportional binding of the Coomassie dye to protein. Bovine

serum albumin (BSA) dissolved in water to a concentration of 4 mg/mL and a serial diluted of BSA standard solutions were prepared. Bradford reagent (Bio-Rad laboratories, USA) was diluted at a 1:5 ratio with water. 20 μ L of the standards (in triplicates) were loaded into a 96-well microtitre plate (Greiner Bio-One, Germany). Solubilized protein samples were diluted 1:10 in RIPA buffer and 20 μ L samples loaded in triplicates into the subsequent columns. Bradford reagent (200 μ L) was added to each well. After incubation for 5 minutes at room temperature, absorbance of the standards and samples were read at 595 nm using an Infinite 200 PRO micro plate reader (Tecan, Maennedorf, Switzerland). The standard curve was plotted and absorbance of the unknown protein sample was calculated from the standard curve.

2.6.4 Bio-Rad DC protein assay

Working reagent A was prepared by adding 20 μ L of reagent S to each mL of reagent A from the Bio-Rad Reagent package (Bio-Rad Laboratories, Inc., Hercules, CA, USA) and mixing thoroughly. Standard used for Bio-Rad DC protein assay was BSA and 2 mg/mL BSA was diluted to make a series of standards containing from 0.2 mg/mL to 1.5 mg/mL protein with the RIPA buffer, which was the same buffer used for protein extraction. The standard curve was constructed from the serial diluted BSA in a range of 0 mg/mL to 1.5 mg/mL. Unknown protein samples can be used directly or diluted five times with RIPA buffer. Standards and unknown samples (5 μ L) were transferred into a 96-well microtiter plate. 25 μ L of working reagent (Reagent A + Reagent S) was then added into each well, followed by 200 μ L Reagent B. The microtiter plate was incubated for 15 minutes with gentle agitation in the dark at room temperature. After removing any bubbles, absorbance readings were read at 750 nm using an Infinite 200 PRO microplate reader (Tecan, Maennedorf, Switzerland). Based on the absorbance of standards, the standard curve was plotted, and the absorbance of unknown protein sample was calculated from the standard curve.

2.6.5 Plate reading

The plate was placed onto an Infinite 200 PRO micro plate reader (Tecan, Maennedorf, Switzerland) with an appropriate absorbance wavelength setting. Standard curves were prepared by measuring the absorbance of BSA in a serial dilution. The calibration curves were linear ($r^2 > 0.99$) over the concentration range tested (0 – 2000 $\mu\text{g/mL}$) and the precision of all standards was reproducible with coefficient of variation, $\text{CV} < 5\%$. The protein concentration was calculated by comparing the absorbance of the known protein BSA standards with those from the unknown samples.

2.6.6 SDS-Polyacrylamide gel electrophoresis (SDS-PAGE)

A Laemmli SDS-polyacrylamide gel was cast using the Bio-Rad Mini-PROTEAN II system. The resolving gel was composed of 12% acrylamide (37.5: 1) in 0.375 M Tris-HCl, pH 8.8 and 0.1% SDS. The stacking gel was composed of 4% acrylamide in 0.125 M Tris-HCl, pH 6.8, and 0.1% SDS. The gels were polymerized by the addition of freshly prepared 0.1% ammonium persulfate and 0.01% Tetramethylethylenediamine (TEMED). Protein samples were mixed with an equal volume of 2x sample buffer (65.8 mM Tris-HCl, pH 6.8, 2.1% SDS, 26.3% (w/v) glycerol, 0.01% bromophenol blue) (Bio-Rad) and heated at 100°C for 10 minutes before being loaded into the gel. Electrophoresis was carried out in 1x running buffer (25 mM Tris, pH 8.3, 192 mM glycine and 0.1% SDS) at a constant voltage of 100 V for 2 hours. After electrophoresis was completed, the gel was removed from the gel cassette sandwich. After cutting off the stacking gel portion, the gel was equilibrated in transfer buffer for two minutes. Meanwhile, the Polyvinylidene Difluoride (PVDF) membrane (Bio-Rad Laboratories, Inc., Hercules, CA, USA), cut to the dimensions of the gel, was incubated in methanol for 1 minute and transferred into transfer buffer for another 3 minutes incubation. The filter paper and fiber pads were soaked in transfer buffer for 5 minutes. The electrophoresis transfer cassette was assembled in the following order: black side of the gel holder cassette; pre-wetted fiber pad; pre-wetted filter paper; gel; membrane; pre-wetted filter

paper; pre-wetted fiber pad; red side of the gel holder cassette. To optimize protein electrophoresis transfer, air bubbles were removed. The cassette was firmly closed and set in buffer tank filled with cold electrophoretic transfer buffer. The proteins separated by SDS-PAGE were transferred from the gels onto PVDF membrane for 2 hours at a constant voltage of 50 V.

2.6.7 Immunodetection of protein

Proteins were resolved in the SDS-PAGE gel and transferred to PVDF membranes. The membranes were blocked with 5% Bovine serum albumin in TBS with 0.1% Tween-20 (TBST) or non-fat dry milk in PBS with 0.1% Tween-20 (PBST) for 2 hours at room temperature. The blots were washed 4 times with PBST for 15 minutes and subsequently immunolabeled with the desired primary antibodies for 2 hours at room temperature or overnight at 4°C (Table 8). After the primary antibodies incubation, the blots were washed 4 times with PBST for 15 minutes and incubated with corresponding secondary Horseradish Peroxidase (HRP)-conjugated IgG antibody diluted in blocking buffer for 1 hour at room temperature. Following incubation, the blots were washed 4 times with PBST for 15 minutes before incubation with the SuperSignal West Pico Chemiluminescent Substrate kit (Thermo Scientific) for 5 minutes in the dark. Blots were then exposed to X-ray film for 1 - 5 minute exposures and the film was developed by Konica SRX-101A processor (Konica Minolta Inc., Tokyo, Japan) for detection of protein band. For re-blotting, membranes were stripped for 5 minutes in stripping buffer (0.2 M NaOH). Blots were washed for 10 minutes with Milli-Q water followed by PBST at room temperature. Blots were blocked with 5% non-fat dry milk in PBS with 0.1% Tween-20 (PBST) for 2 hour at room temperature. Thereafter, blots were immunolabeled with loading control such as β -actin monoclonal antibody. The procedure for immunodetection of the loading control was the same as described above. The recommended antibodies dilutions were listed in Table 10.

Table 8: Antibodies

Antibody	Supplier	Molecular weight (kDa)	Recommended dilution
VEGF-A	C-1: sc-7269, Santa Cruz Biotechnology	21/42	1:2000
TFF3	Anti-PGM 3 (animal 3105) polyclonal antibody was generated by Amiry <i>et al.</i> (2009) and synthesized by Biogenes, GmbH D, Berlin	7	1:2000
pSTAT3	B-7: sc-8058, Santa Cruz Biotechnology	86/91	1:2000
STAT3	C-20: sc-482, Santa Cruz Biotechnology	86/91	1:3000
IL-8	MAB-208, R&D systems	8	1:2000

2.5.8 Densitometric analysis of intensity of band

The amplified PCR products resolved in the agarose gel were captured by GelDoc imaging system (Bio-Rad) and intensity of the band of interest was analyzed by QuantityOne program (version 1.0.1, Bio-Rad). The protein bands developed in X-ray film were captured and analyzed by ImageJ. Bands of interest in the agarose gel or X-ray films were marked and their total integrated volumes were quantified against the background. Density was the corrected intensity integrated with volumes (in arbitrary units).

2.6 *In vivo* study

2.6.1 Angiogenesis *in vivo* assay

The angiogenesis *in vivo* assay using tumor xenograft models was performed in collaboration with Dr Tao Zhu (University of Science and Technology of China, Hefei). All the *in vivo* work related to mice models were performed under a standard protocol approved by the institutional animal care and use committee. MCF7-Vec and MCF7-TFF3 (5×10^6) were suspended in 100 μ L Matrigel and injected into the first mammary (axillary) fat pad of six-week-old athymic (nu/nu) mice (Shanghai Slaccas Co.). Tumor xenografts produced by MCF7-Vec and MCF7-TFF3 were dissected and stored at -80°C for immunohistochemical (IHC) analysis and protein extraction. Tumor sections were prepared by fixing the tumor

tissues in 4% PFA (pH 7.4) overnight, embedded in paraffin, and cut into less than 5- μ m thick paraffin (or frozen) sections. For IHC analysis, tissue sections of the tumors were mounted on glass slides, deparaffinised and rehydrated. The slides were rehydrated and incubated with 3% hydrogen peroxide for 30 minutes. The sections were blocked with 10% goat serum (Sigma) in PBS for 30 minutes and then incubated at room temperature for 90 minutes with the following antibodies: Anti-mouse CD31 (550274, BD) (1:100 dilution), anti-CD34/podoplanin (ab11936, abcam) (1:200 dilution), and anti-IL-8 antibody (R&D System) (1:100 dilution). The sections were washed with PBS and incubated with the respective biotinylated secondary antibodies such as anti-mouse IgG (BA-9200) or anti-rabbit IgG (BA-100) (1:300 dilution) at room temperature for 1 hour. Subsequently, an Elite ABC immunoperoxidase kit (PK-6100 vector Laboratory) was added to the sections and incubated for 30 minutes at room temperature, followed by visualization with diaminobenzidine (DAB) (ImmPACT DAB Substrate SK-4105 vector lab) (1 - 10 minutes at room temperature). Finally, the slides were mounted in DakoCytomation fluorescent mounting media and observed under a microscope (OLYMPUS AX70). Five different fields were chosen randomly from seven sections of each xenograft across the whole tumor. Photographs were captured with identical settings for all sections. Statistical analysis of protein expression was determined as previously described (Araneda *et al.*, 2005). A common threshold level was selected for all analyzed images to prevent intra-assay variations and the background level of the control sections was calculated for image analysis. ImageJ Program, version 1.45s (National Institute of Health, USA) was used to analyze the images (JPEG or TIFF files).

2.7 Bioinformatics Tools

2.7.1 Software for statistical analysis

The statistics software program Sigma Stat 3.1 was used in conjunction with Microsoft Excel for statistical analyses. The graphical presentations were generated using GraphPad Prism 5 (GraphPad Software, Inc., CA, USA). All experiments were performed for

three or four times. Numerical data were expressed as mean \pm SEM of triplicate determinants. Experiments were repeated for three times and data were analyzed by unpaired two-tailed student's *t* test or analysis of variance (ANOVA). A representative figure for each experiment is shown.

2.7.2 BLAST

Basic Local Alignment Search Tool (BLAST) was utilized for both DNA and protein sequence database searches (Altschul *et al.*, 1990). The basic algorithms of BLAST were used for gene identification searches, gene alignment searches, as well as transcription start site (TSS) estimations of various genes with uncharacterized promoter regions, specifically utilizing the EST-search function. BLAST was accessed via the National Centre for Biotechnology Information (NCBI). Website: <http://www.ncbi.nlm.nih.gov/BLAST/>.

CHAPTER 3

TFF3 Promotes *de novo* Angiogenesis in Mammary Carcinoma

3.1 Introduction

De novo angiogenesis is associated with tumor growth and metastasis (Schneider and Miller, 2005, Fox *et al.*, 2007, Paez-Ribes *et al.*, 2009). Adequate vascularization of the tumor is required for delivery of nutrients and oxygen to the growing tumor (Folkman, 1985, Risau, 1997). In a tumor microenvironment, the tumor is deprived of oxygen because of its distance from the nearest blood vessels and this hypoxic environment triggers the cancer cells to produce angiogenic factors or growth factors (Bergers and Benjamin, 2003, Gelao *et al.*, 2013). Angiogenic factors secreted from tumors or stromal cells stimulate neovascularization by activating endothelial cell proliferation, migration, survival, and degradation of cell to cell contact and cell to matrix adhesion (Gupta and Qin, 2003). Establishment of highly permeable and disorganized vasculatures in the tumor facilitates dissemination of cancer cells through the bloodstream to distant organs to form metastases (Baeriswyl and Christofori, 2009, Valastyan and Weinberg, 2011). Importantly, the survival and proliferation of the tumor depends on angiogenesis that is mediated by numerous of angiogenic factors, particularly vascular endothelial growth factors (VEGF) (Ferrara, 2004, Ferrara, 2005, Shibuya, 2008) and interleukin 8 (IL-8) (Koch *et al.*, 1992, Ning *et al.*, 2010).

A number of studies have reported that TFF3 expression was significantly associated with pro-survival and pro-invasive activities of mammary carcinoma cells (Emami *et al.*, 2001, Rodrigues *et al.*, 2003a, Kannan *et al.*, 2010, Ahmed *et al.*, 2012). Increased TFF3 expression in mammary carcinoma cells promoted cell proliferation, survival, oncogenicity, migration and invasion. (Kannan *et al.*, 2010, Ahmed *et al.*, 2012, Pandey *et al.*, 2014). TFF3 mRNA expression has been demonstrated to predict micrometastatic mammary carcinoma (Weigelt *et al.*, 2004, Mikhitarian *et al.*, 2005). The gene expression of TFF1 and TFF3 are associated with metastasis of breast cancer as reported by a microarray analysis of breast

cancer tissues (Smid *et al.*, 2006). Another recent studies displayed similar observations, increased TFF3 expression promotes metastasis and predicts poor survival outcomes of patients with mammary carcinoma (Kannan *et al.*, 2010, Pandey *et al.*, 2014). Inevitably, TFF3 may serve as an independent predictive biomarker for metastasis of mammary carcinoma.

In addition to its metastatic properties, TFF3 has recently been identified as a potential pro-angiogenic factor implicated in tumor angiogenesis. Immunohistochemical (IHC) analysis of tumor tissues has demonstrated that increased TFF3 expression was positively correlated with enhanced microvessel density (vessels labeled with CD31 marker) in gastric carcinoma (Dhar *et al.*, 2005) and breast carcinoma (Ahmed *et al.*, 2012). These observations were concordant with a study by Rodrigues *et al.* (2003b) who demonstrated that recombinant human TFF3 induced vessel formation in a chick chorioallantoic membrane (CAM) assay. However, the role of TFF3 in *de novo* angiogenesis in mammary carcinoma has not been determined.

IL-8 is a potent angiogenic factor involved in angiogenesis and metastasis of mammary carcinoma (Basolo *et al.*, 1993, Green *et al.*, 1997, Youngs *et al.*, 1997, De Larco *et al.*, 2001). It has been reported that elevated expression of IL-8 in mammary carcinoma cells was correlated with metastatic potential and tumor angiogenesis (Lin *et al.*, 2004). A clinical study has reported that triple negative (ER-PR-HER2-) breast cancer patients with elevated IL-8 expression were characterized by increasing invasiveness and metastatic potential that contributed to high risk of recurrence and poor prognosis (Rody *et al.*, 2011). The IL-8 serum concentration in patients with advanced breast cancer was higher than that of healthy subjects. Increased IL-8 expression was associated with worse survival outcome, a higher tumor load, and involvement of liver or lymph node (Benoy *et al.*, 2004). The presence of bone metastasis in patients with advanced breast cancer was positively correlated with increased IL-8 expression (Simeone *et al.*, 2007), suggesting that IL-8 is an independent

predictive marker for breast cancer patients with high metastatic capacity and poor survival outcome (De Larco *et al.*, 2003, Simeone *et al.*, 2007).

It has also been shown that IL-8 and its cognate receptors namely CXCR1 and CXCR2 were positively associated with poor prognosis in patients with breast cancer (Miller *et al.*, 1998, Benoy *et al.*, 2004). The ability of IL-8 to elicit angiogenic activity depends on the expression of its receptors by endothelial cells (Singh *et al.*, 2010). IL-8 stimulates endothelial cell proliferation and capillary tube formation in a concentration-dependent manner, and these angiogenic effects can be abrogated by monoclonal antibodies inhibitory to IL-8 (Heidemann *et al.*, 2003, Li *et al.*, 2005). Neutralizing antibodies to CXCR1 and CXCR2 inhibit migration of endothelial cells promoted by IL-8, suggesting that these two receptors are critical for activation of the angiogenic responses of IL-8 (Salcedo *et al.*, 2000a, Li *et al.*, 2005). Tumor cells exploit the expression of IL-8 and its receptors to enhance tumor progression through regulation tumor growth, angiogenesis, and immune response. Increased IL-8 expression alters the tumor microenvironment to be favorable for cancer cells to metastasize and colonize at the targeted organs (Yuan *et al.*, 2005, Singh *et al.*, 2010, Lee *et al.*, 2012). Inhibition of IL-8 by humanized anti-IL-8 antibodies attenuated tumor growth, angiogenesis and metastasis of human melanoma (Huang *et al.*, 2002). Administration of a humanized monoclonal antibody against IL-8 has been shown to suppress the growth of bladder cancer in xenograft models (Mian *et al.*, 2003).

IL-8 signaling activated growth factor receptors and stimulated the activity of MAPK signaling cascade, which is related to the promoting effect of IL-8 on cell proliferation and survival of cancer (Brew *et al.*, 2000, Luppi *et al.*, 2007) and endothelial cell lines (Li *et al.*, 2003a, Waugh and Wilson, 2008). It is known that PI3K is involved in the regulation of IL-8. Activation of PI3K/Akt signaling pathway is modulated by IL-8 to promote cell survival, angiogenesis, and migration of mammary carcinoma cells (Cheng *et al.*, 2008, Waugh and Wilson, 2008, Todorović-Raković and Milovanović, 2013). IL-8 signaling is likely to promote the transcriptional activity of multiple genes that involved in angiogenesis, migration,

invasion and the evasion of apoptosis (Waugh and Wilson, 2008). In addition to IL-8, VEGF-A and TFF3 were connected to signal transducers and activators of transcription 3 (STAT3) signaling as these two peptides promote activation of STAT3 by tyrosine phosphorylation at 705 amino acid residues (Rivat *et al.*, 2005, Pandey *et al.*, 2014). As a result, the expression of TFF3 and VEGF-A was up-regulated by STAT3 (Niu *et al.*, 2002, Tebbutt *et al.*, 2002). The persistent STAT3 activity enhanced by growth factors as well as additional oncogenes which promote oncogenic transformation and invasion of cancer cells such as Src family kinases and RhoA (Turkson *et al.*, 1998, Simon *et al.*, 2000, Goiot *et al.*, 2001). The activated dimeric STAT3 translocates into the nucleus, where it binds to the targeted DNA response elements within the promoter region of a specific gene and subsequently activate its gene transcription (Horvath *et al.*, 1995, Darnell, 1997). TFF peptides directly induced cell scattering and cellular invasion of kidney and colonic carcinoma cells through autocrine loops (Emami *et al.*, 2001). Alternatively, the pro-invasive activity of TFF3 was controlled by activation of Src and Rho-dependent signaling pathways that led to tyrosine phosphorylation of STAT3, suggesting that STAT3 may be a crucial transcription factor involved in the mechanistic action of TFF peptides (Emami *et al.*, 2001). A recent study observed that TFF3 expression in mammary carcinoma cells stimulated tyrosine phosphorylation of c-Src, which subsequently increased STAT3 activity and led to the down-regulation of E-cadherin to promote cell invasion (Pandey *et al.*, 2014). Blockade of STAT3 signaling by a dominant-negative element (STAT3 β), depletion of STAT3 by siRNA and inhibition of STAT3 activation by STAT3 inhibitory peptide abrogated cellular invasion and growth of colon cancer in xenograft models (Rivat *et al.*, 2005). Inhibition of STAT3 activity using STAT3 inhibitors and depletion of STAT3 by siRNA largely inhibited the ability of TFF3 to stimulate invasion of mammary carcinoma cells (Pandey *et al.*, 2014).

The persistent STAT3 activity exhibits anti-apoptotic, mitogenic, and angiogenic effects in cancer cells. STAT3 stimulates tumor angiogenesis by increasing the promoter activity of VEGF-A (Bromberg *et al.*, 1999, Shen *et al.*, 2001, Niu *et al.*, 2002). Furthermore,

STAT3 has been suggested as a regulator of IL-8 at the transcriptional level by direct binding to the IL-8 promoter (Oka *et al.*, 2010). However, the underlying mechanism by which TFF3 promote *de novo* angiogenesis in mammary carcinoma has not yet been determined. The role of STAT3 in TFF3-stimulated angiogenesis in mammary carcinoma remains elusive. I postulate that a similar STAT3 signaling pathway between TFF3 and the TFF3-stimulated pro-angiogenic factor, which can be a target gene of STAT3 and coordinately mediates TFF3 to promote angiogenesis in mammary carcinoma. Herein, I have determined the effect of TFF3 secreted from mammary carcinoma cells on the angiogenic behaviors of endothelial cells to promote *de novo* angiogenesis in mammary carcinoma and delineated the underlying mechanism by which TFF3 promotes *de novo* angiogenesis in mammary carcinoma.

In this study, I utilized two human mammary adenocarcinoma cell lines, namely MCF-7 and T47D cells, as *in vitro* models, by stable forced expression of TFF3 or depletion of TFF3 in these cell lines. These cell lines are easily propagated and are amenable to genetic manipulation (Masters, 2000). Additionally, these cell lines can be implanted into immunodeficient mice as xenograft models and the effects of altered gene function and pharmacological inhibition of tumorigenicity in breast cancer both *in vitro* and *in vivo* can be determined (Lacroix and Leclercq, 2004). Additionally, the effect of TFF3 secreted from mammary carcinoma cells on endothelial cells was determined by using an indirect co-culture transwell system, in which mammary carcinoma cells plated on the membrane of transwell inserts were co-cultured with endothelial cells seeded in the bottom well of the companion plate. This indirect co-culture system enables two different type of cells to culture together, which is mimic to the *in vivo* situation and allows the soluble factors from mammary carcinoma cells to diffuse through the pore of the membrane to the endothelial cells and subsequently modulate the angiogenic behaviors of endothelial cells. To examine the angiogenic potential of TFF3, a tubule formation assay was performed in which mammary carcinoma cells plated on the membrane of transwell inserts co-cultured with endothelial cells seeded in the Matrigel coated in the bottom well of the companion plate. Tubules formed by

HUVEC in the Matrigel can be quantified to assess the angiogenic activity of TFF3 on the endothelial cells (Bishop *et al.*, 1999) and the morphology of tubules generated by endothelial cells is representative of capillary vessel formation *in vivo* (Donovan *et al.*, 2001, Bagley *et al.*, 2003). By using this approach, the roles of TFF3 secreted from mammary carcinoma cells on the angiogenic activities of HUVEC can be determined.

3.2 Results

3.2.1 Expression of TFF3 mRNA in mammary carcinoma cells

The expression of TFF3 mRNA in several ER+ mammary carcinoma cell lines (MCF-7, T47D, MDA-MB-361, and BT474) and one ER- mammary carcinoma cell line (MDA-MB-231) were analyzed by semi-quantitative RT-PCR. ER+ mammary carcinoma cell lines expressed higher TFF3 mRNA as compared to the ER- mammary carcinoma cell line (MDA-MB-231) (Figure 22A). The expression of TFF3 in mammary carcinoma cell lines was consistent with the previous studies reported that TFF3 was associated with ER status (May and Westley, 1997a, Doane *et al.*, 2006, Pandey *et al.*, 2014). MCF-7 and T47D cells expressed moderate levels of TFF3 mRNA were chosen to be utilized as mammary carcinoma cell models (Kannan *et al.*, 2010, Pandey *et al.*, 2014).

A RT-PCR

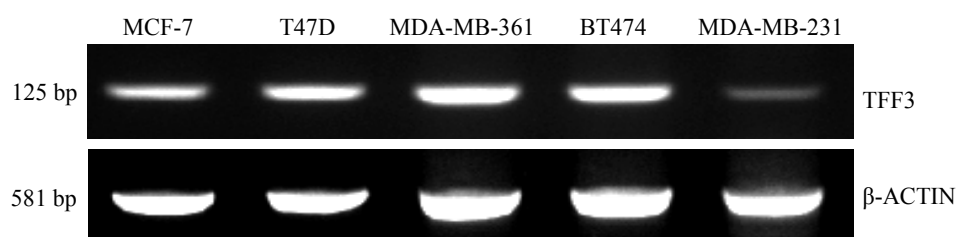


Figure 22: TFF3 mRNA expression in several of mammary carcinoma cell lines. A, Semi-quantitative RT-PCR analysis of TFF3 mRNA expression in several mammary carcinoma cell lines including MCF-7, T47D, MDA-MB-316, and BT474 (ER+ mammary carcinoma cells) and MDA-MB-231 (ER- mammary carcinoma cells). β-ACTIN was used as a loading control in semi-quantitative RT-PCR and Western blot analysis.

3.2.2 Forced expression of TFF3 in mammary carcinoma cells increased TFF3 expression

To determine the stimulatory effect of TFF3 secreted from human mammary carcinoma cells on the angiogenic behavior of HUVEC, MCF-7 and T47D cells were stably transfected with a pIRESneo3 expression vector containing TFF3 cDNA (designated as MCF7-TFF3 and T47D-TFF3) or a pIRESneo3 empty vector (designated as MCF7-Vec and T47D-Vec). The expression of TFF3 mRNA and protein in MCF-7 and T47D with forced expression of TFF3 was verified by semi-quantitative RT-PCR and Western blot analyses. Forced expression of TFF3 in MCF-7 and T47D cells increased TFF3 mRNA (Figure 23A-B) and TFF3 protein (Figure 23C-D) when compared with the respective control MCF7-Vec and T47D-Vec.

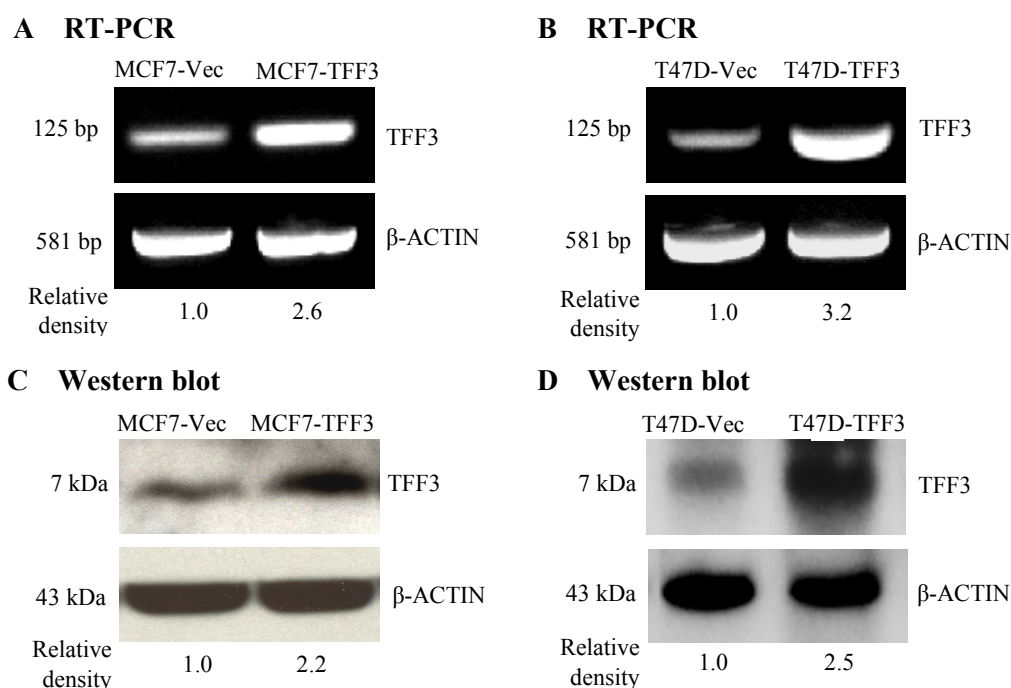


Figure 23: Forced expression of TFF3 in mammary carcinoma cells increased TFF3 expression. A-B, semi-quantitative RT-PCR analysis of TFF3 mRNA in MCF-7 and T47D cells with forced expression of TFF3. C-D, Western blot analysis of TFF3 protein in MCF-7 and T47D cells with forced expression of TFF3. β-ACTIN was used as a loading control in both semi-quantitative RT-PCR and Western blot analysis.

3.2.3 Forced expression of TFF3 in mammary carcinoma cells promoted HUVEC monolayer proliferation, cell cycle progression, and survival

A previous study has reported that TFF3 secreted from human mammary carcinoma cells is oncogenic and promoted proliferation of mammary carcinoma cells *in vitro* and increased tumor growth in xenograft models *in vivo* (Kannan *et al.*, 2010). Therefore, the stimulatory effect of TFF3 secreted from mammary carcinoma cells on the angiogenic activities of HUVEC was determined by using an indirect co-culture system, in which MCF7-TFF3 and T47D-TFF3 were plated on the membrane of the transwell inserts (0.4 μ m membrane pores) and co-cultured with HUVEC seeded in the bottom well of the companion plate. Co-culturing HUVEC with MCF7-TFF3 and T47D-TFF3 increased HUVEC monolayer proliferation in both 10% FBS conditions for 72 hours and 0.2% FBS conditions for 48 hours, when compared with HUVEC co-cultured with respective control MCF7-Vec and T47D-Vec. TFF3 secreted from MCF7-TFF3 and T47D-TFF3 increased HUVEC monolayer proliferation by 35% and 40%, respectively after 72 hours when compared with the respective control cells (Figure 24A-B). TFF3 secreted from MCF7-TFF3 and T47D-TFF3 promoted a small increase of HUVEC monolayer proliferation by 12% and 13%, respectively after 48 hours when compared with the respective control cells (Figure 24C-D). TFF3 secreted from mammary carcinoma cells promoted HUVEC monolayer proliferation.

Endothelial cell proliferation and survival are the most essential components to support and maintain vasculature in the tumor (Nor *et al.*, 1999). Increased monolayer cell proliferation is achieved by increased cell cycle progression and/or decreased apoptotic cell death. The effect of TFF3 secreted from mammary carcinoma cells on HUVEC cell cycle progression and apoptotic cell death was determined by co-culturing HUVEC with MCF7-TFF3 and T47D-TFF3. Cell cycle progression was analyzed by 5-bromo-2-deoxyuridine (BrdU) incorporation assay. BrdU labeling is as a marker of DNA synthesis. BrdU can be incorporated into nuclear DNA during the S-phase of the cell cycle as a substitute for thymidine during DNA replication (Miller and Nowakowski, 1988). TFF3 secreted from

MCF7-TFF3 and T47D-TFF3 increased HUVEC cell cycle progression in serum-free conditions by 28% and 21%, respectively when compared with the respective control cells. TFF3 secreted from MCF7-TFF3 and T47D-TFF3 significantly increased HUVEC proliferation in 10% FBS conditions by 43% and 21%, respectively when compared with the respective control cells (Figure 25A-B). TFF3 secreted from MCF-7 and T47D with forced expression of TFF3 promoted HUVEC cell cycle proliferation in both serum-free and 10% FBS conditions.

In addition to cell proliferation, resistance to apoptosis is the other essential component for the survival of endothelial cells. TFF3 secreted from MCF7-TFF3 and T47D-TFF3 significantly decreased HUVEC apoptotic cell death by 52% and 39%, respectively when compared with the respective control cells in serum-free conditions. TFF3 secreted from MCF7-TFF3 and T47D-TFF3 decreased HUVEC apoptotic cell death by 61% and 50% respectively when compared with the respective control cells in 10% FBS conditions (Figure 25C-D). TFF3 secreted from mammary carcinoma cells inhibited HUVEC apoptotic cell death in both serum-free and 10% FBS conditions. Additionally, TFF3 secreted from mammary carcinoma cells protected HUVEC from apoptosis induced by serum starvation. Therefore, TFF3 secreted from mammary carcinoma cells promoted proliferation of HUVEC by increased cell cycle progression and decreased apoptotic cell death.

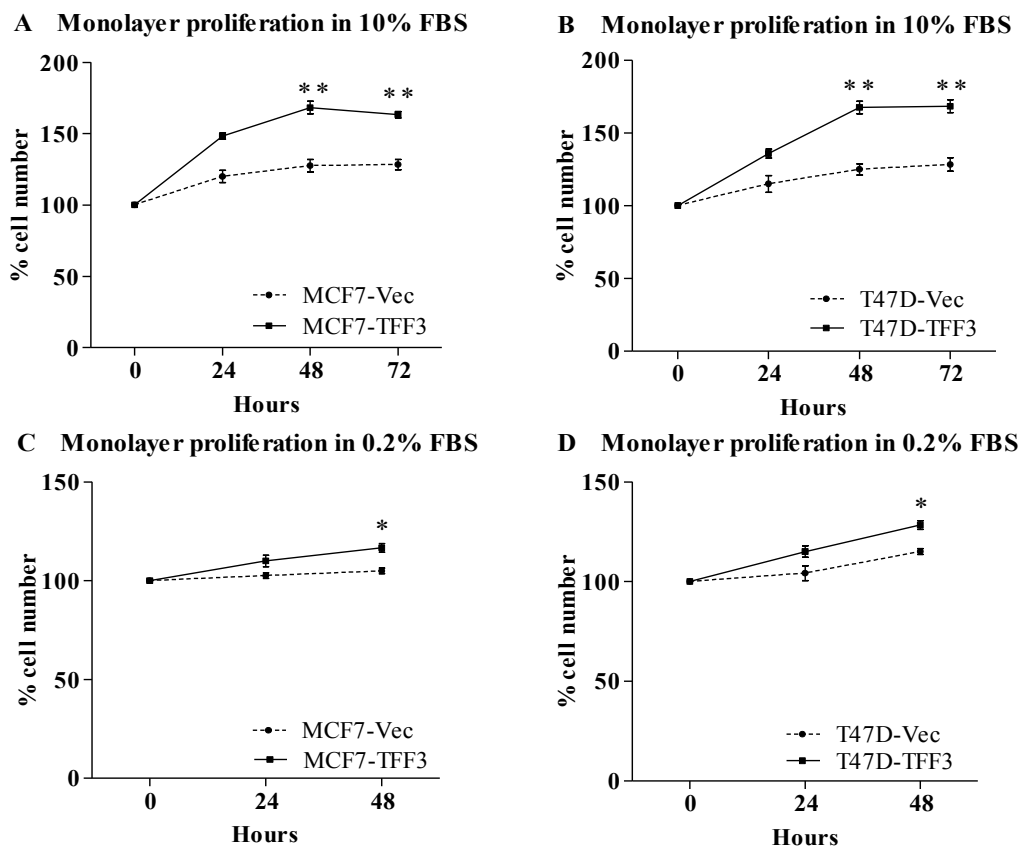


Figure 24: Forced expression of TFF3 in mammary carcinoma cells increased HUVEC monolayer proliferation. A, monolayer proliferation of HUVEC after co-culture with MCF-7 cells with forced expression of TFF3 in 10% FBS conditions. MCF-7 cells with empty vector were used as control. B, monolayer proliferation of HUVEC after co-culture with T47D cells with forced expression of TFF3 in 10% FBS conditions. T47D cells with empty vector were used as control. C, monolayer proliferation of HUVEC after co-culture with MCF-7 cells with forced expression of TFF3 in 0.2% FBS conditions. D, monolayer proliferation of HUVEC after co-culture with T47D cells with forced expression of TFF3 in 0.2% FBS conditions. *, $P < 0.05$; **, $P < 0.01$.

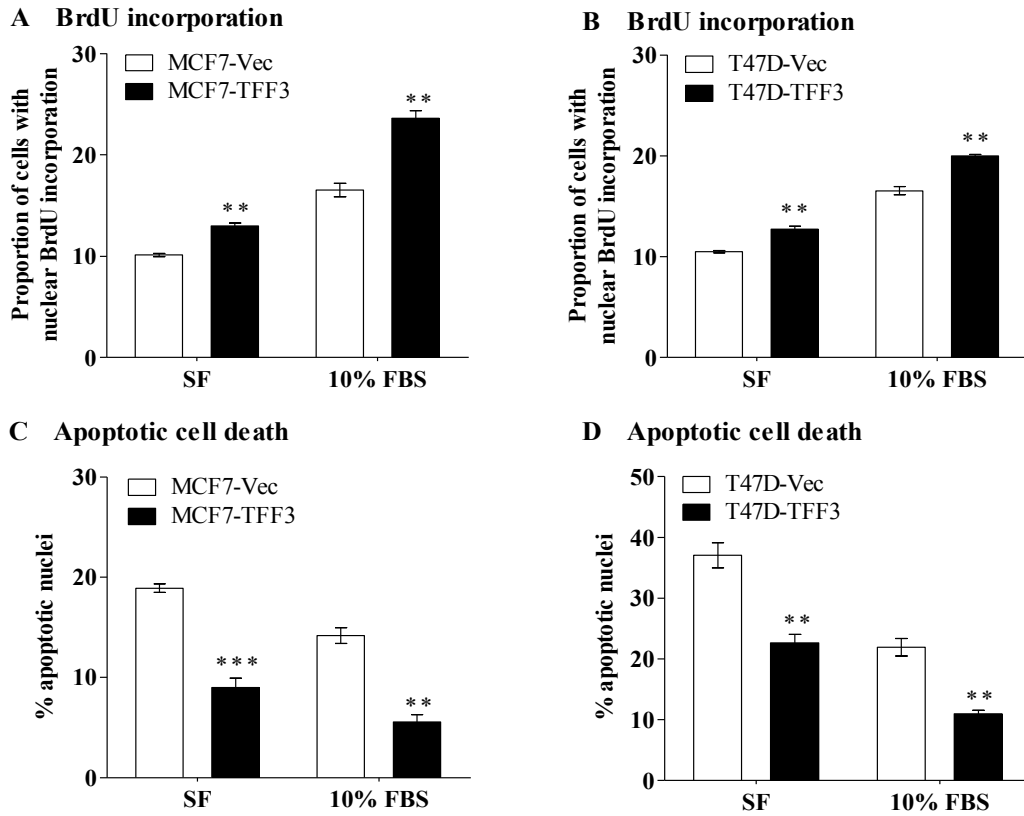


Figure 25: Forced expression of TFF3 in mammary carcinoma cells increased HUVEC cell cycle progression and survival. A, HUVEC cell cycle progression after 24 hours co-culture with MCF-7 cells with forced expression of TFF3 in serum-free (SF) and 10% FBS conditions. MCF-7 cells with empty vector were used as control. B, HUVEC cell cycle progression after 24 hours co-culture with T47D with forced expression of TFF3 in serum-free (SF) and 10% FBS conditions. T47D cells with empty vector were used as control. C, HUVEC apoptotic cell death after 24 hours co-culture with MCF-7 cells with forced expression of TFF3 in serum-free (SF) and 10% FBS conditions. D, HUVEC apoptotic cell death after 24 hours co-culture with T47D cells with forced expression of TFF3 in serum-free (SF) and 10% FBS conditions. **, $P < 0.01$; ***, $P < 0.001$.

3.2.4 Forced expression of TFF3 in mammary carcinoma cells promoted HUVEC migration, invasion, and tubule formation *in vitro*

During the process of *de novo* tumor angiogenesis, the surrounding tissue are invaded by endothelial cells to generate neovascularization the tumor (Lamallice *et al.*, 2007). I therefore determined the effects of TFF3 secreted from mammary carcinoma cells on the migratory and invasive behavior of HUVEC. Transwell migration and invasion assays were conducted in which HUVEC seeded on the membrane of transwell inserts (8.0 μ m membrane

pore) were co-cultured with MCF-7 and T47D with forced expression of TFF3 plated in the bottom well of companion plate. TFF3 secreted from MCF7-TFF3 and T47D-TFF3 significantly increased HUVEC migration by 121% and 100%, respectively as compared to the respective control cells (Figure 26A-B). Additionally, TFF3 secreted from MCF7-TFF3 and T47D-TFF3 significantly increased HUVEC invasion by 80% and 98% respectively as compared to the respective control cells (Figure 26C-D). TFF3 secreted from mammary carcinoma cells promoted HUVEC migration and invasion.

HUVEC retains the ability to form three-dimensional tubules in the Matrigel thereby stimulating angiogenesis *in vitro* (Bouïs *et al.*, 2001, Bagley *et al.*, 2003). The morphology of tubules formed by HUVEC in the Matrigel is representative of the capillary vessel formation *in vivo* (Donovan *et al.*, 2001, Bagley *et al.*, 2003). To determine if TFF3 secreted from mammary carcinoma cells stimulated angiogenic behavior of HUVEC, a tubule formation assay was conducted in which mammary carcinoma cells with forced expression of TFF3 were plated on the membrane of transwell insert co-cultured with HUVEC seeded in the Matrigel that coated in the bottom well of the companion plate. TFF3 secreted from MCF7-TFF3 and T47D-TFF3 significantly increased tubule length and tubule number when compared with the respective control cells. TFF3 secreted from MCF7-TFF3 and T47D-TFF3 increased tubule length by 72% and 41%, respectively (Figure 27A-C) and tubule number by 28% and 30%, respectively (Figure 27B-D) when compared with the respective control cells. Co-culturing HUVEC with MCF7-TFF3 and T47D-TFF3 increased tubules formed by HUVEC in the Matrigel when compared with HUVEC co-cultured with the respective control cells (Figure 27E-F). Therefore, TFF3 secreted from mammary carcinoma cells promoted HUVEC tubule formation *in vitro*

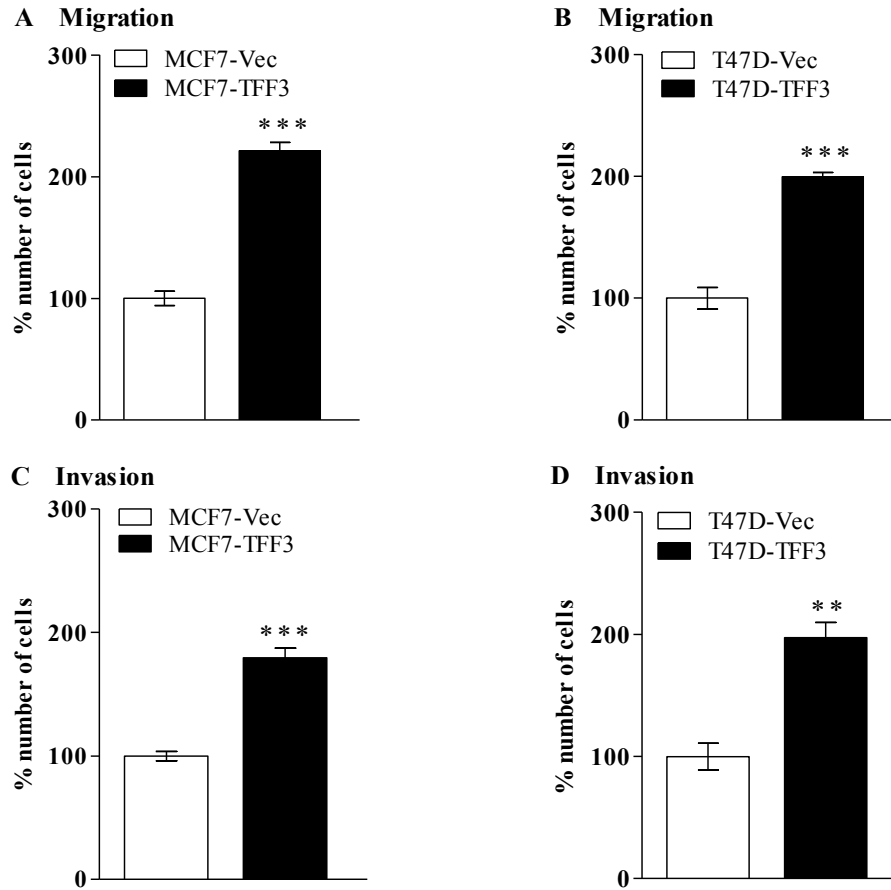


Figure 26: Forced expression of TFF3 in mammary carcinoma cells increased HUVEC migration and invasion. A, HUVEC migration after 24 hours co-culture with MCF-7 cells with forced expression of TFF3 in serum-free conditions. MCF-7 cells with empty vector were used as control. B, HUVEC migration after 24 hours co-culture with T47D cells with forced expression of TFF3 in serum-free conditions. T47D cells with empty vector were used as control. C, HUVEC invasion after 24 hours co-culture with MCF-7 cells with forced expression of TFF3 in serum-free conditions. D, HUVEC invasion after 24 hours co-culture with T47D cells with forced expression of TFF3 in serum-free conditions. **, $P < 0.01$; ***, $P < 0.001$.

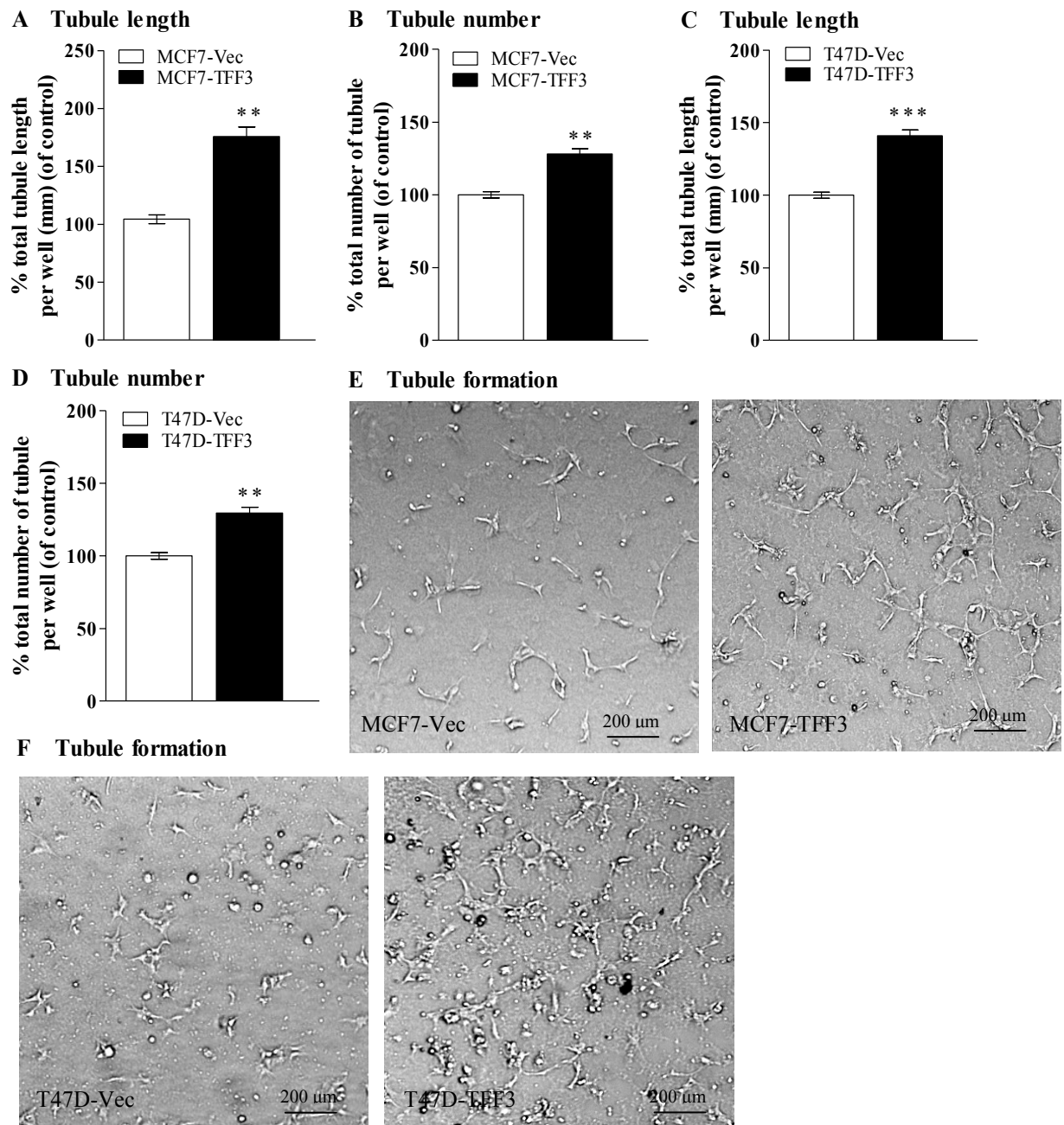
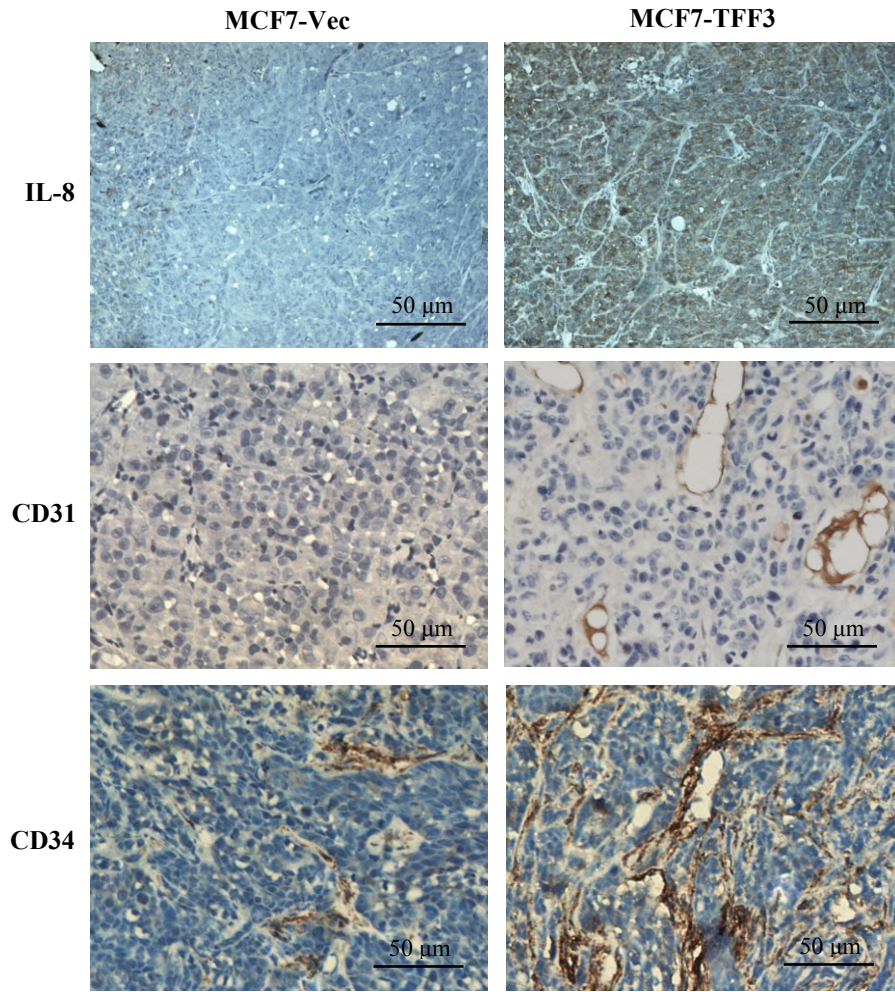


Figure 27: Forced expression of TFF3 in mammary carcinoma cells increased HUVEC tubule formation *in vitro*. A-B, HUVEC tubule formation *in vitro* on Matrigel after 12 hours co-culture with MCF-7 cells with forced expression of TFF3. MCF-7 cells with empty vector were used as control. Total tubule length (A) and total tubule number (B) were assessed. C and D, HUVEC tubule formation *in vitro* on Matrigel after 12 hours co-culture with T47D cells with forced expression of TFF3. T47D cells with empty vector were used as control. Total tubule length (C) and total tubule number (D) were assessed using ImageJ analysis software. E and F, representative light microscopy images of HUVEC tubule formation *in vitro* in the Matrigel after 12 hours co-culture with MCF-7 and T47D cells with forced expression of TFF3. The light microscopy images were taken at $\times 40$ magnification. **, $P < 0.01$; ***, $P < 0.001$; scale bar, 200 μm .

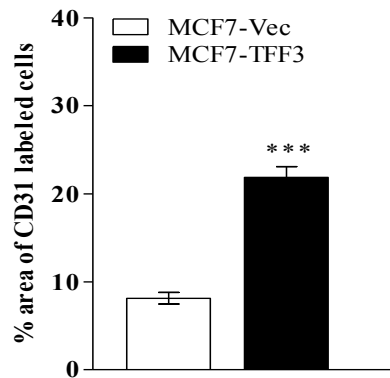
3.2.5 Forced expression of TFF3 in mammary carcinoma cells promoted angiogenesis *in vivo*

To determine the potential *in vivo* role of TFF3 in *de novo* angiogenesis in mammary carcinoma, MCF7-Vec or MCF7-TFF3 cells were implanted into the mammary fat pad of immunodeficient nude mice and allowed to grow for 28 days. As previously reported, the tumors produced by MCF7-TFF3 were larger than those formed by MCF7-Vec. After 4 weeks, indicating that TFF3 enhanced tumorigenicity *in vivo* (Kannan *et al.*, 2010). The proteins expression of IL-8, CD31, and CD34 in xenografts derived from MCF7-TFF3 and control MCF7-Vec were examined by IHC analysis. In xenograft models, MCF-7 cells with forced expression of TFF3 produced tumors with increased the expression of IL-8 protein as compared to tumors formed by control cells (Figure 28A), suggesting that TFF3 secreted from MCF-7 cells with forced expression of TFF3 promoted IL-8 protein expression. Tumor vasculature formed in xenografts was determined by analyzing microvessel density, which can be quantified by the area of CD31 and/or CD34 labeled cells. Endothelial cell surface marker, CD31 is an indicator of angiogenesis, cells expressing CD31 have higher angiogenic properties (Kim *et al.*, 2010). MCF-7 cells with forced expression of TFF3 produced tumors with increased area of CD31 labeled cells as compared to tumors formed by control cells (Figure 28A-B), indicating TFF3 secreted from mammary carcinoma cells significantly increased tumor microvessel density. CD34 (podoplanin) is a small transmembrane protein of lymphatic endothelium and molecular marker of lymphangiogenesis (Kahn and Marks, 2002). Lymphatic vasculature was determined by analyzing the area of CD34-labeled cells. IHC analysis demonstrated that a significantly increase area of CD34 labeled cells in tumors derived from MCF7-TFF3 when compared with tumors derived from control MCF7-Vec (Figure 28A-C), indicating that TFF3 secreted from mammary carcinoma cells increased lymphatic vascularization. These observations suggested that TFF3 secreted from mammary carcinoma cells promoted angiogenesis *in vivo*.

A IHC analysis



B CD31



C CD34

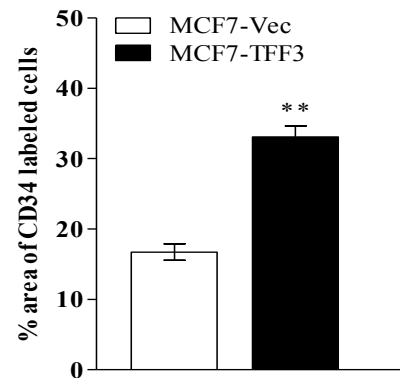


Figure 28: Forced expression of TFF3 in mammary carcinoma cells promoted angiogenesis *in vivo*. A, IHC analysis of IL-8, CD31, and CD34 proteins expression in xenograft tumors produced by control MCF7-Vec and MCF7-TFF3. B, Microvessel density (CD31) was assessed by quantifying percentage area of CD31 labeled cells in xenografts formed by control MCF7-Vec and MCF7-TFF3. C, CD34 was assessed by quantifying percentage area of CD34 labeled cells in xenografts formed by control MCF7-Vec and MCF7-TFF3. **, $P < 0.01$; ***, $P < 0.001$.

3.2.6 Depletion of TFF3 in mammary carcinoma cells by siRNA decreased TFF3 expression

The effects of depletion of endogenous TFF3 in mammary carcinoma cells on angiogenic behavior of HUVEC were also determined. MCF-7 and T47D cells were transiently transfected with a pSilencer 2.1-U6 hygro expression vector containing TFF3 siRNA (designated as MCF7-siTFF3 and T47D-siTFF3) or with a pSilencer 2.1-U6 hygro empty vector containing control siRNA (designated as MCF7-siVec and T47D-siVec) (Pandey *et al.*, 2014). The expression of TFF3 mRNA and protein in MCF-7 and T47D cells with depletion of TFF3 was verified by semi-quantitative RT-PCR and Western blot analysis. Depletion of TFF3 by siRNA in MCF-7 and T47D cells decreased TFF3 mRNA (Figure 29A-B) and decreased TFF3 protein (Figure 29C-D) when compared with the respective control cells. These data indicated that the endogenous expression of TFF3 in MCF-7 and T47D cells was depleted by siRNA.

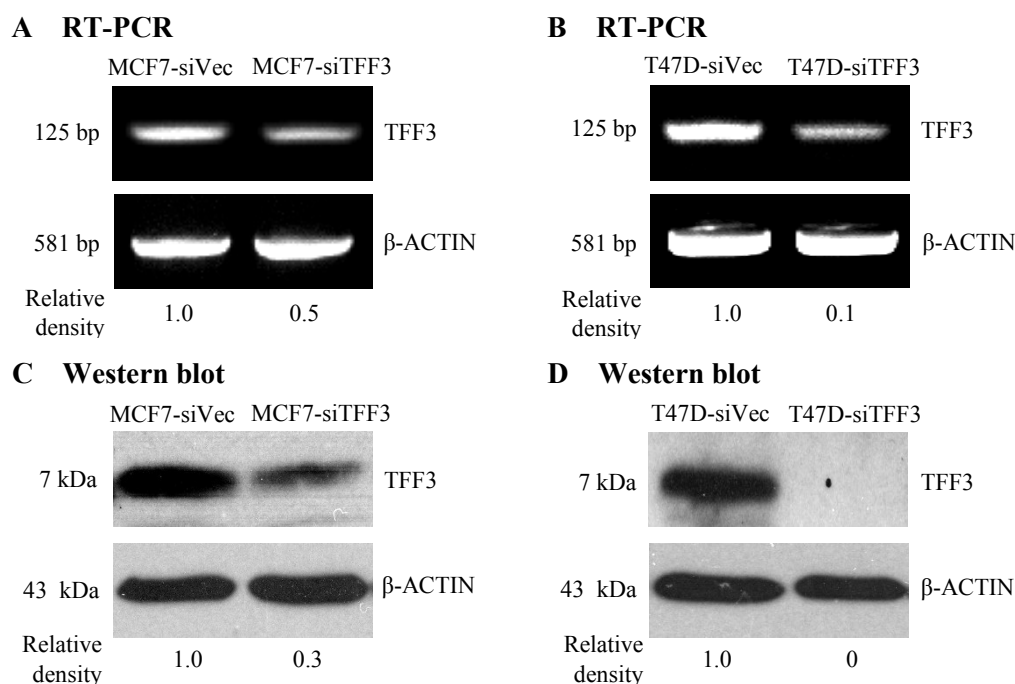


Figure 29: Depletion of TFF3 in mammary carcinoma cells decreased TFF3 expression. A, semi-quantitative RT-PCR analysis of the TFF3 mRNA expression in MCF-7 cells with depletion of TFF3. B, semi-quantitative RT-PCR analysis of the TFF3 mRNA expression in T47D cells with depletion of TFF3. C, Western blot analysis of TFF3 protein in MCF-7 cells with depletion of TFF3. D, Western blot analysis of TFF3 protein in T47D cells with depletion of TFF3. β -ACTIN was used as a loading control in both semi-quantitative RT-PCR and Western blot analysis.

3.2.7 Depletion of TFF3 in mammary carcinoma cells decreased HUVEC monolayer proliferation, cell cycle progression and survival

The effect of depletion of TFF3 in mammary carcinoma cells on HUVEC proliferation and survival were determined by co-culturing HUVEC with mammary carcinoma cells with depletion of TFF3. When compared with the respective control cells co-cultured with HUVEC, depletion of TFF3 in MCF-7 and T47D cells decreased HUVEC monolayer proliferation when compared with the respective control cells, in both 10% FBS conditions for 72 hours and 0.2% FBS conditions for 48 hours, respectively. Depletion of TFF3 by siRNA in MCF-7 and T47D cells significantly decreased HUVEC monolayer proliferation in 10% FBS conditions by 48% and 43%, respectively after 72 hours when compared with the respective control cells (Figure 30A-B). MCF-7 and T47D cells with depletion of TFF3 decreased HUVEC monolayer proliferation in 0.2% FBS condition by 18%

and 25%, respectively after 48 hours as compared with the respective control cells (Figure 30C-D). Depletion of TFF3 in mammary carcinoma cells decreased HUVEC monolayer cell proliferation.

Co-culturing HUVEC with MCF-7 and T47D cells with depletion of TFF3 significantly decreased HUVEC cell cycle progression, in both serum-free and 10% FBS conditions, when compared with HUVEC co-cultured with the respective control cells. Depletion of TFF3 by siRNA in MCF-7 and T47D cells significantly decreased HUVEC cell cycle progression in serum-free conditions by 27% and 30%, respectively as compared with the respective control cells (Figure 31A-B). MCF-7 and T47D cells with depletion of TFF3 significantly decreased HUVEC cell proliferation in 10% FBS conditions by 32% or 26%, respectively as compared with the respective control cells (Figure 31A-B). Furthermore, co-culture of HUVEC with MCF-7 and T47D cells with depletion of TFF3 significantly increased HUVEC apoptotic cell death in both serum-free and 10% FBS conditions, when compared with HUVEC co-cultured with the respective control cells. Depletion of TFF3 by siRNA in MCF-7 and T47D cells significantly increased HUVEC apoptotic cell death in serum-free conditions by 53% and 50%, respectively as compared with the respective control cells (Figure 31C-D). MCF-7 and T47D cells with depletion of TFF3 significantly increased HUVEC apoptotic cell death in 10% FBS conditions by 50% and 43%, respectively as compared with the respective control cells (Figure 31C-D). Depletion of TFF3 in mammary carcinoma cells by siRNA diminished HUVEC proliferation and survival.

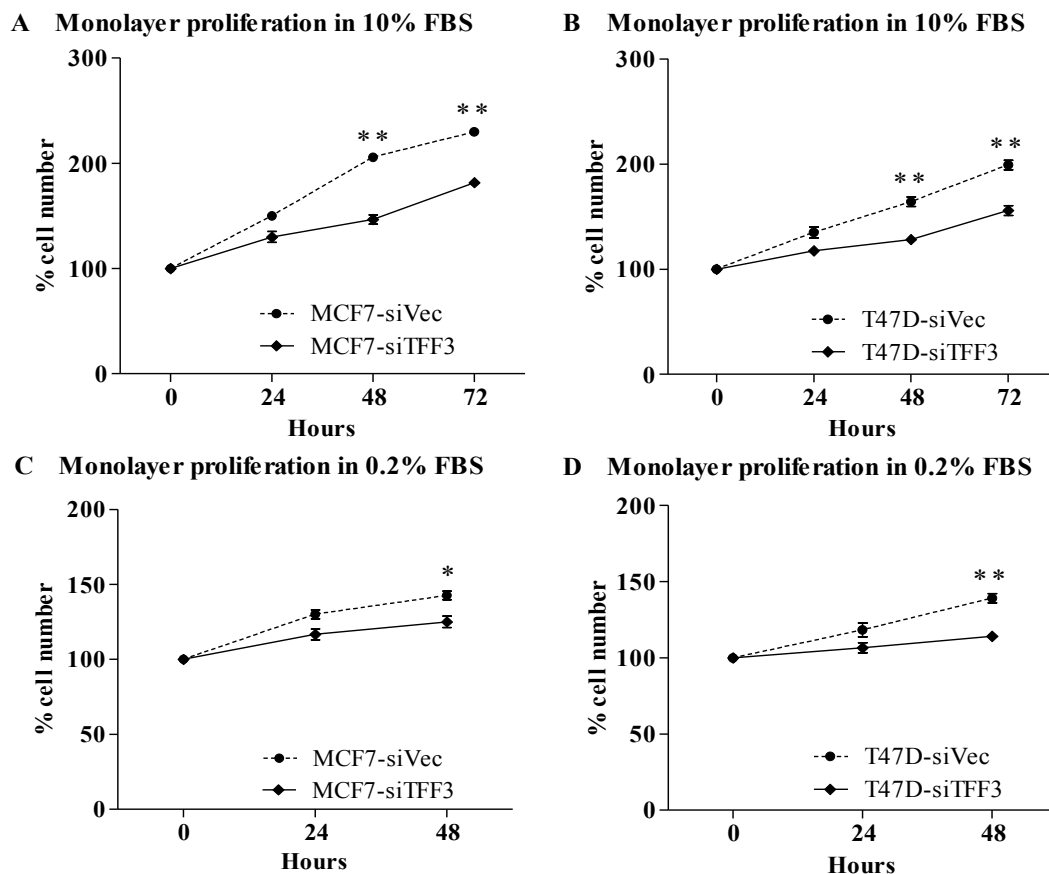


Figure 30: Depletion of TFF3 in mammary carcinoma cells decreased HUVEC monolayer proliferation. A, HUVEC monolayer proliferation after co-culture with MCF-7 cells with depletion of TFF3 in 10% FBS conditions. MCF-7 cells with siRNA control vector were used as control. B, HUVEC monolayer proliferation after co-culture with T47D cells with depletion of TFF3 in 10% FBS conditions. MCF-7 cells with siRNA control vector were used as control. C, HUVEC monolayer proliferation after co-culture with MCF-7 cells with depletion of TFF3 in 0.2% FBS conditions. D, HUVEC monolayer proliferation after co-culture with T47D cells with depletion of TFF3 in 0.2% FBS conditions. *, $P < 0.05$. **, $P < 0.01$.

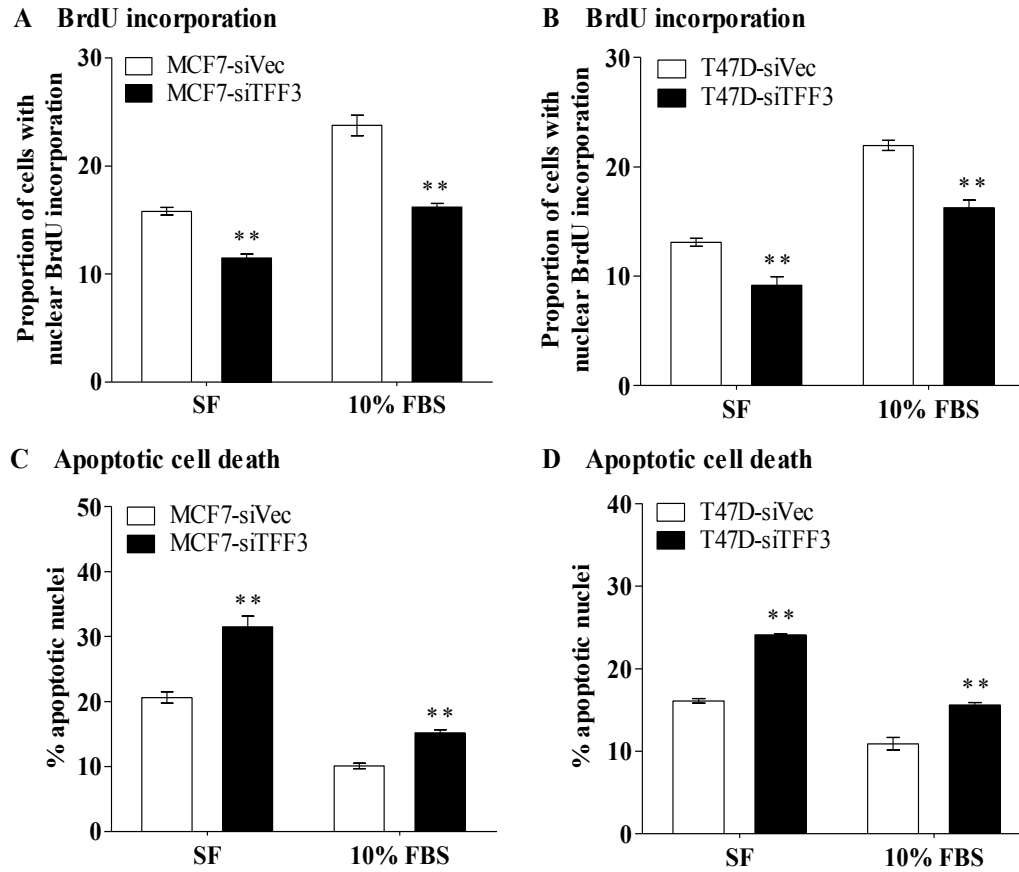


Figure 31: Depletion of TFF3 in mammary carcinoma cells decreased HUVEC cell cycle progression and survival. A, HUVEC cell cycle progression after 24 hours co-culture with MCF-7 cells with depletion of TFF3 in serum-free (SF) and 10% FBS conditions. MCF-7 cells with siRNA control vector were used as control. B, HUVEC cell cycle progression after 24 hours co-culture with T47D cells with depletion of TFF3 in serum-free (SF) and 10% FBS conditions. T47D cells with siRNA control vector were used as control. C, HUVEC apoptotic cell death after 24 hours co-culture with MCF-7 cells with depletion of TFF3 in serum-free (SF) and 10% FBS conditions. D, HUVEC apoptotic cell death after 24 hours co-culture with T47D cells with depletion of TFF3 in serum-free (SF) and 10% FBS conditions. **, $P < 0.01$.

3.2.8 Depletion of TFF3 in mammary carcinoma cells decreased HUVEC migration, invasion, and tube formation *in vitro*

The effect of depletion of TFF3 in mammary carcinoma cells on the migratory and invasive behavior of endothelial cells were determined by co-culturing HUVEC with mammary carcinoma cells with depletion of TFF3. Depletion of TFF3 in MCF-7 and T47D cells significantly decreased HUVEC migration by 41% and 45%, respectively (Figure 32A-B) and HUVEC invasion by 36% and 33%, respectively as compared with the respective control cells (Figure 32C-D). These data indicated that depletion of TFF3 diminished HUVEC migration and invasion.

To determine the effect of depletion of TFF3 by siRNA in mammary carcinoma cells on the angiogenic behaviors of HUVEC, a tubule formation assay was conducted by co-culturing depletion of TFF3 in MCF-7 and T47D cells with HUVEC seeded in the Matrigel. Depletion of TFF3 in MCF-7 and T47D cells by siRNA significantly decreased tubule length by 46% and 36%, respectively (Figure 33A-C) and tubule number by 38% and 30%, respectively (Figure 33B-D) when compared with the respective control cells. Depletion of TFF3 in MCF-7 and T47D cells decreased tubules formed by HUVEC in the Matrigel when compared with the respective control cells (Figure 33E-F). These data indicated that depletion of TFF3 inhibited HUVEC tubule formation *in vitro*. Depletion of TFF3 by siRNA in mammary carcinoma cells diminished angiogenic behaviors of HUVEC.

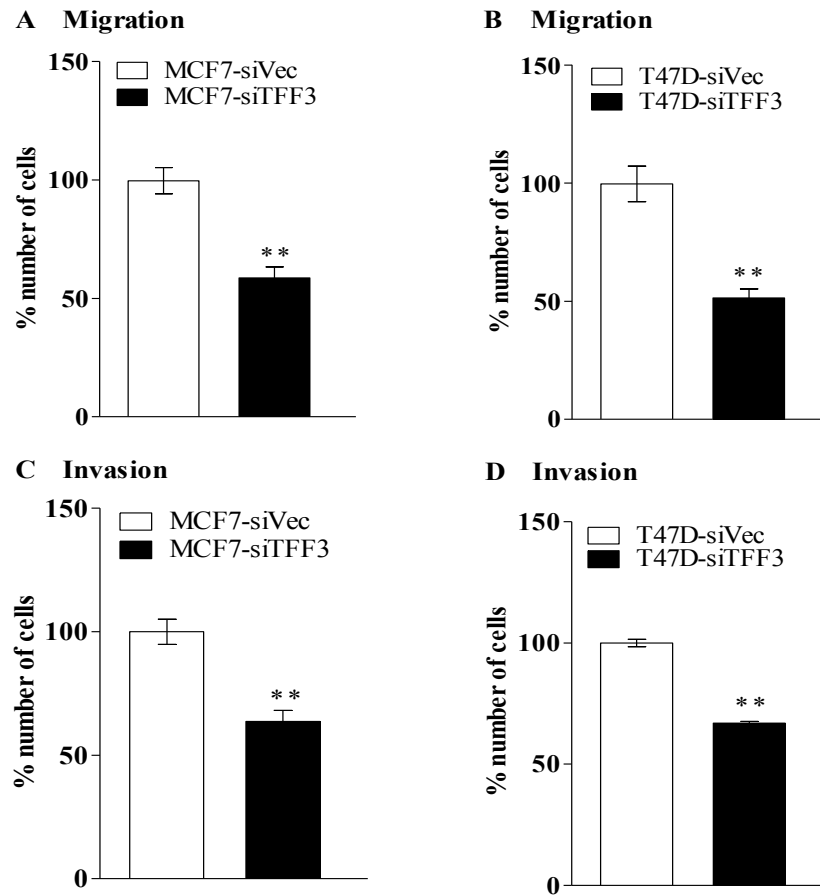


Figure 32: Depletion of TFF3 in mammary carcinoma cells decreased HUVEC migration and invasion. A, HUVEC migration after 24 hours co-culture with MCF-7 cells with depletion of TFF3. MCF-7 cells with siRNA control vector were used as control. B, HUVEC migration after 24 hours co-culture with T47D cells with depletion of TFF3. T47D cells with siRNA control vector were used as control. C, HUVEC invasion after 24 hours co-culture with MCF-7 cells with depletion of TFF3. D, HUVEC invasion after 24 hours co-culture with T47D cells with depletion of TFF3. **, $P < 0.01$.

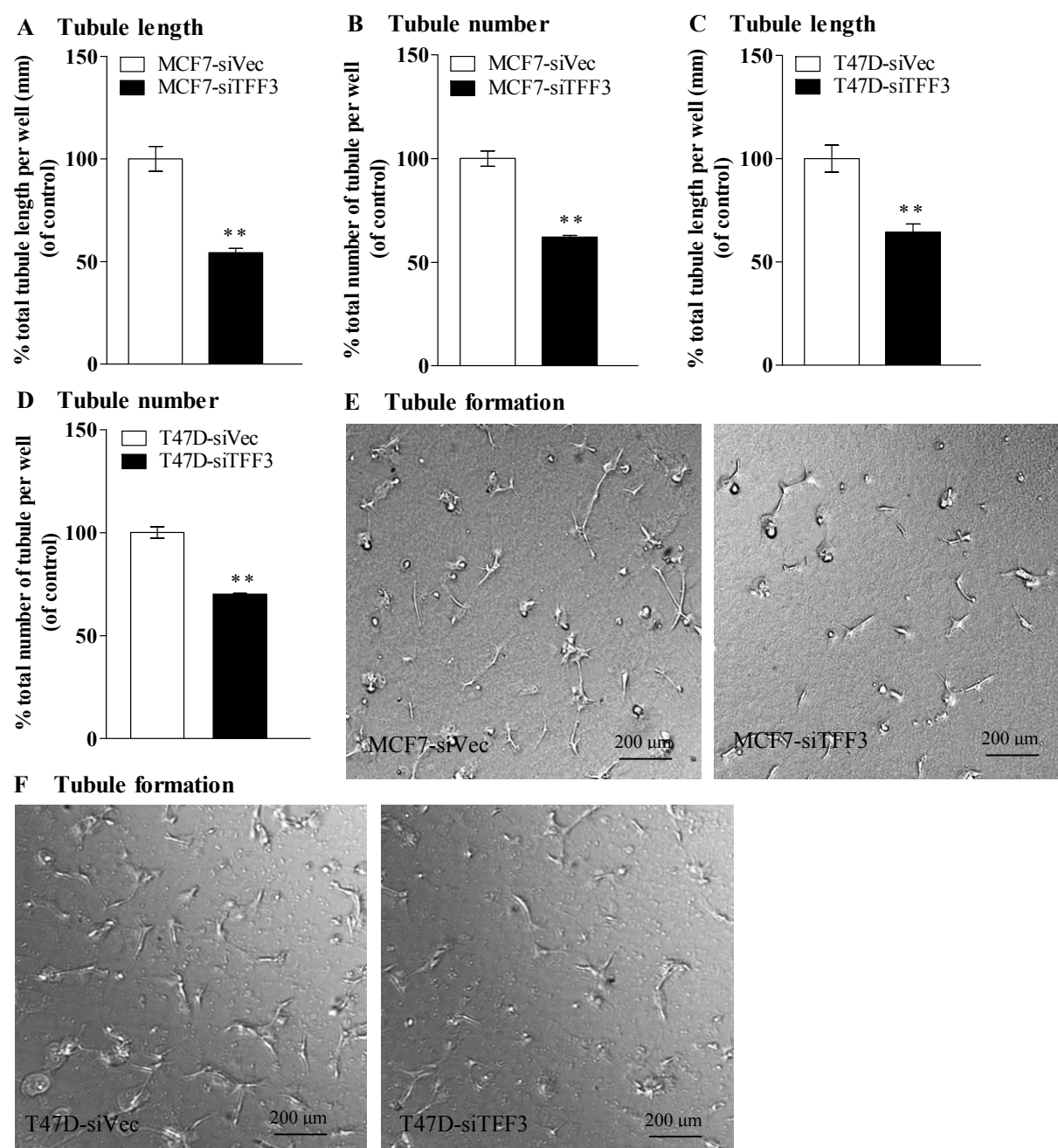


Figure 33: Depletion of TFF3 in mammary carcinoma cells decreased HUVEC tubule formation *in vitro*. A and B, HUVEC tubule formation *in vitro* on Matrigel after 12 hours co-culture with MCF-7 cell with depletion of TFF3 in serum-free conditions. MCF-7 cells with siRNA control vector were used as control. Total tubule length (A) and tubule number (B) were assessed after 12 hours incubation. C and D, HUVEC tubule formation *in vitro* on Matrigel after 12 hours co-culture with T47D cells with depletion of TFF3 in serum-free conditions. T47D cells with siRNA control vector were used as control. Total tubule length (C) and tubule number (D) were assessed after 12 hours incubation using ImageJ analysis software. E and F, representative light microscopy images of HUVEC tubule formation *in vitro* on Matrigel after 12 hours co-culture with MCF-7 and T47D cells with depletion of TFF3. The light microscopy images were taken at $\times 40$ magnification. **, $P < 0.01$; scale bar, 200 μm .

3.2.9 Forced expression of TFF3 in mammary carcinoma cells increased IL-8 expression

According to the previously published microarray data set (Gene Expression Omnibus accession number GSE3494) (Miller *et al.*, 2005) as well as the gene expression profiling of MCF-7 with forced expression of TFF3 (Kannan *et al.*, 2010), several angiogenic markers associated with tumor angiogenesis were selected for further validation using real-time qPCR analysis. The qPCR analysis showed that forced expression of TFF3 in MCF-7 cells significantly increased the gene expression of VEGF-A (1.8-fold increase), IL-8 (5.5-fold increase) and transforming growth factor-beta (TGFB) (11.4-fold increase) as compared with the control MCF7-Vec (Figure 34). High level of TGF-beta is observed at the edges of breast tumor spread and is correlated with lymph node metastases (Dalal *et al.*, 1993). TGF-beta exhibits dual roles in promoting and suppression of tumor formation (Lebrun, 2012). It has previously reported that the motogenic activity of TFF3 for epithelial cells was not associated with alteration in the concentrations of TGF-beta protein and not affected by the presence of anti-TGF beta antibody (Dignass *et al.*, 1994). Hence, IL-8 was selected for further investigation the role of IL-8 in mammary carcinoma angiogenesis stimulated by TFF3. The expression of VEGF-A and IL-8 in mammary carcinoma cells with forced expression of TFF3 was analyzed by semi-quantitative RT-PCR and Western blot or ELISA analysis. The qPCR analysis showed that the VEGF-A gene expression was slightly up-regulated by TFF3, but the expression of VEGF-A mRNA in MCF-7 cells with forced expression of TFF3 appeared to be not markedly different from the control MCF7-Vec (Figure 35A). This discrepancy probably due to the semi-quantitative RT-PCR was not able to detect the relative differences. The protein expression of VEGF-A in MCF-7 cells with forced expression of TFF3 was relatively similar to the control MCF7-Vec (Figure 35B). This result indicated that the expression of VEGF-A was probably not regulated by TFF3. Mammary carcinoma cells endogenously expressed relatively low level of IL-8 mRNA (Figure 35C), but forced expression of TFF3 in MCF-7 and T47D cells increased IL-8 mRNA

level (Figure 35D-E) and increased IL-8 protein secreted to the medium (Figure 35F-G) as compared with the respective control cells. These data suggested that TFF3 stimulated the expression of IL-8 in mammary carcinoma cells.

The functional receptors for IL-8, CXCR1 and CXCR2, are present in different cells including tumors and endothelial cells, and have been demonstrated to involve in tumor angiogenesis (Richards *et al.*, 1997, Kitadai *et al.*, 1998, Miller *et al.*, 1998). Besides over-expression of IL-8, the differential expression of IL-8 receptors in benign and malignant breast tissues has been reported (Miller *et al.*, 1998). The expression of CXCR1 and CXCR2 mRNAs were observed in the mammary carcinoma cells with forced expression of TFF3 (Figure 36A-B).

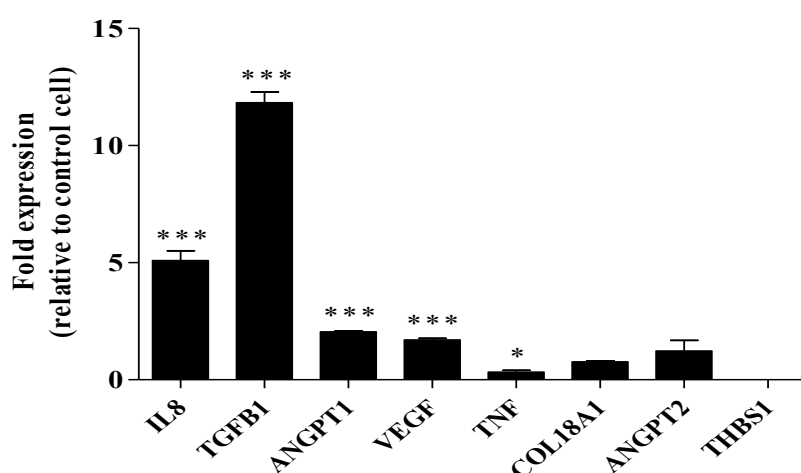


Figure 34: Real-time qPCR analysis of the gene expression of angiogenic markers modulated by TFF3. Fold expression indicated gene expression of angiogenic markers in MCF-7 cells with forced expression of TFF3 relative to control MCF7-Vec. Fold expression ≥ 2 indicated the gene expression of angiogenic markers was up-regulated by TFF3. *, $P < 0.05$; ***, $P < 0.001$. Pro-angiogenic markers included IL-8, interleukin 8; TGFB, Transforming growth factor beta; ANGPT1, Angiopoietin 1; VEGF-A, Vascular endothelial growth factor; TNF; Tumor necrosis factor and anti-angiogenic markers included COL18A1, Collagen alpha-1(XVIII) chain; ANGPT2, Angiopoietin 2; THBS1, Thrombospondin 1.

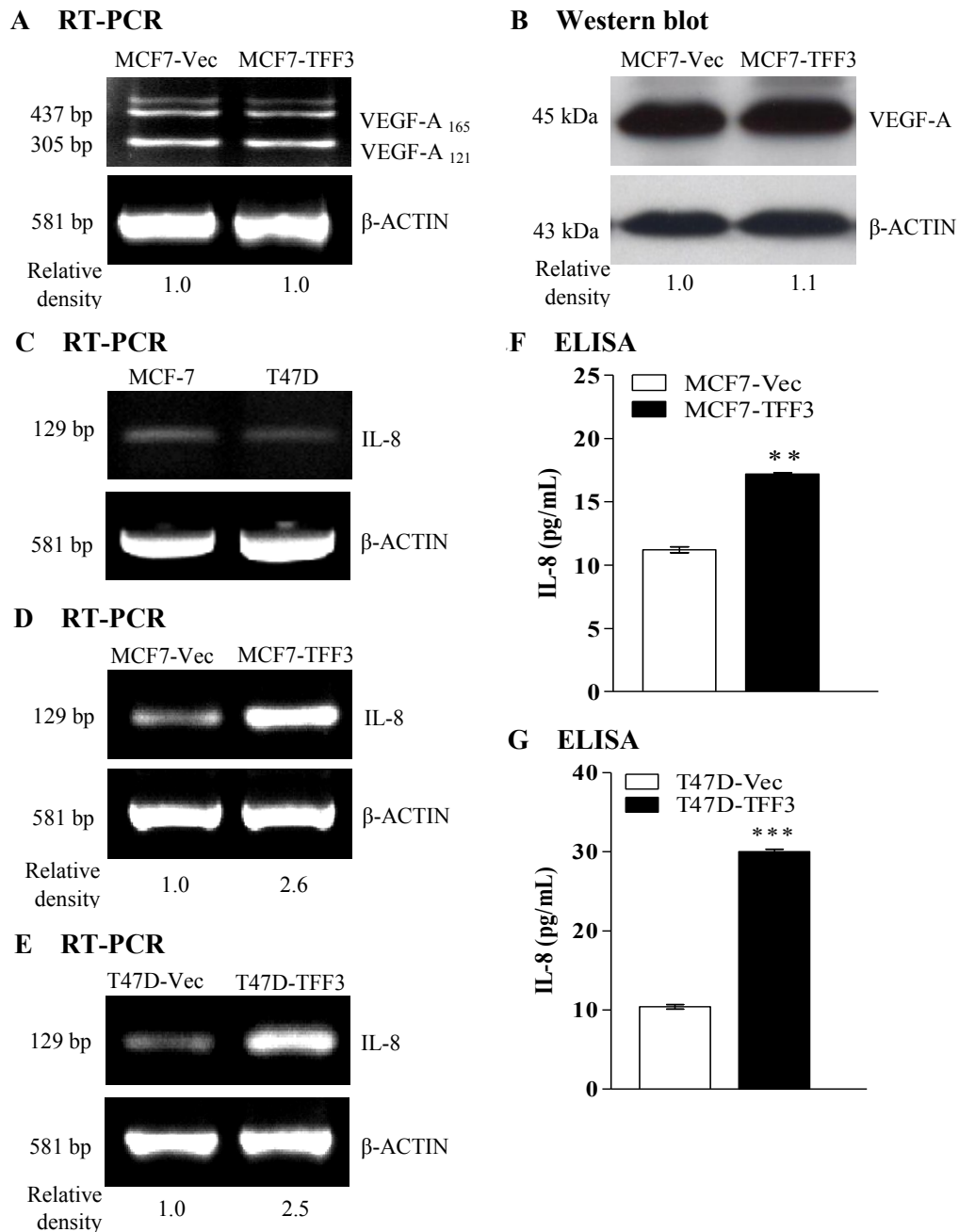


Figure 35: Forced expression of TFF3 in mammary carcinoma cells increased IL-8 expression. A, semi-quantitative RT-PCR analysis of VEGF-A mRNA level in MCF-7 cells with forced expression of TFF3. MCF-7 cells with empty vector were used as control. B, Western blot analysis of VEGF-A protein in MCF-7 cells with forced expression of TFF3. C, semi-quantitative RT-PCR analysis of endogenous expression of IL-8 mRNA in MCF-7 and T47D cells. D, semi-quantitative RT-PCR analysis of the expression of IL-8 mRNA in MCF-7 with forced expression of TFF3. E, semi-quantitative RT-PCR analysis of the expression of IL-8 mRNA in T47D cells with forced expression of TFF3. T47D cells with empty vector were used as control. F, ELISA analysis of IL-8 protein secreted to the medium by MCF-7 cells with forced expression of TFF3. G, ELISA analysis of IL-8 protein secreted to the medium by T47D cells with forced expression of TFF3. β -ACTIN was used as a loading control in both semi-quantitative RT-PCR and Western blot. **, $P < 0.01$, ***, $P < 0.001$.

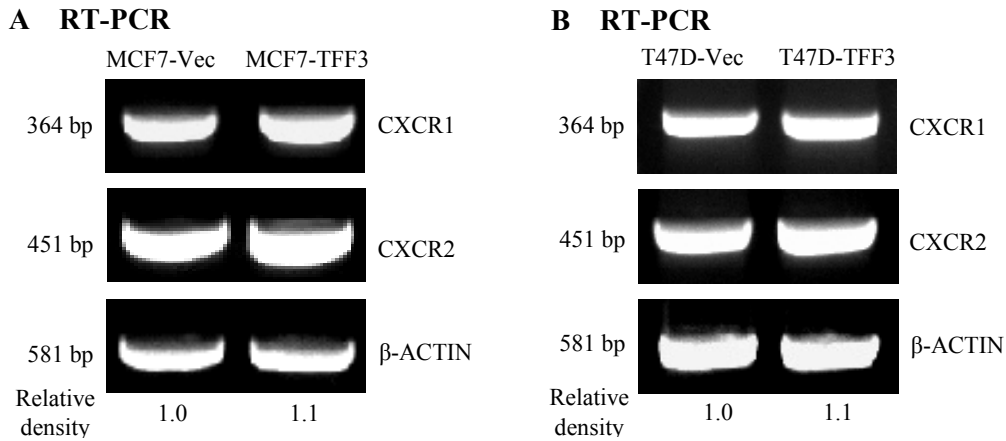


Figure 36: Expression of CXCR1 and CXCR2 mRNA in mammary carcinoma cells with forced expression of TFF3. A, semi-quantitative RT-PCR analysis of the expression of CXCR1 and CXCR2 mRNA in MCF-7 cells with forced expression of TFF3. MCF-7 cells with empty vector were used as control. B, semi-quantitative RT-PCR analysis of the expression of CXCR1 and CXCR2 mRNA in T47D cells with forced expression of TFF3. T47D cells with empty vector were used as control. β -ACTIN was used as a loading control in semi-quantitative RT-PCR.

3.2.10 Forced expression of TFF3 in mammary carcinoma cells increased IL-8 promoter activity

IL-8 protein is secreted in normal tissue to maintain homeostasis, but its expression is rapidly increased in response to pro-inflammatory cytokines or growth factors. The production of IL-8 is regulated by the combinatorial activation of transcription factors and their interaction with the IL-8 promoter gene (Lakshminarayanan *et al.*, 1998, Roebuck *et al.*, 1999). It is known that the proximal region of IL-8 promoter contains functional binding sites for the transcription factors namely NF-IL-6 (-94 to -81 bp), AP-1 (-126 to -120 bp) and NF- κ B (-80 to -70 bp) (Mukaida *et al.*, 1994). Besides these binding sites, additional potential binding sites for STAT3 (-245 to -237 bp) have also been identified (Oka *et al.*, 2010). Firstly, I determined if TFF3 stimulates IL-8 promoter activity, MCF-7 and T47D cells with forced expression of TFF3 were transiently transfected with a full length of IL-8 promoter reporter vector (full length, -4800 to + 104 bp) and a pRL-CMV control reporter vector. MCF-7 and T47D cells with forced expression of TFF3 significantly increased IL-8 promoter activity by 4.5-fold and 2.2-fold respectively when compared with the respective control cells (Figure

37A-B), indicating that TFF3 stimulated IL-8 promoter activity in mammary carcinoma cells. The cooperative actions of NF- κ B, AP-1, and NF-IL-6 transcription factors increase the expression of IL-8 protein (Mukaida *et al.*, 1990, Mukaida *et al.*, 1994, Roebuck, 1999). Secondly, I determined if these transcription factors are involved in enhancing IL-8 promoter activity in mammary carcinoma cells stimulated by TFF3, MCF-7 and T47D with forced expression of TFF3 were transiently transfected with a shorter IL-8 promoter, pGL-IL8-152 reporter vector (-152 to +44 bp) containing transcription factors namely NF- κ B, AP-1, and NF-IL-6 , and a pRL-CMV control reporter vector. MCF-7 and T47D cells with forced expression of TFF3 increased IL-8 promoter activity when compared with the respective control MCF7-Vec and T47D-Vec transiently transfected with pGL-IL8-152 reporter vector (Figure 37C-D). The binding sites for AP-1, NF-IL-6 and NF- κ B, present at the proximal region of IL-8 promoter, were also involved in enhancing IL-8 promoter activity stimulated by TFF3 in mammary carcinoma cells.

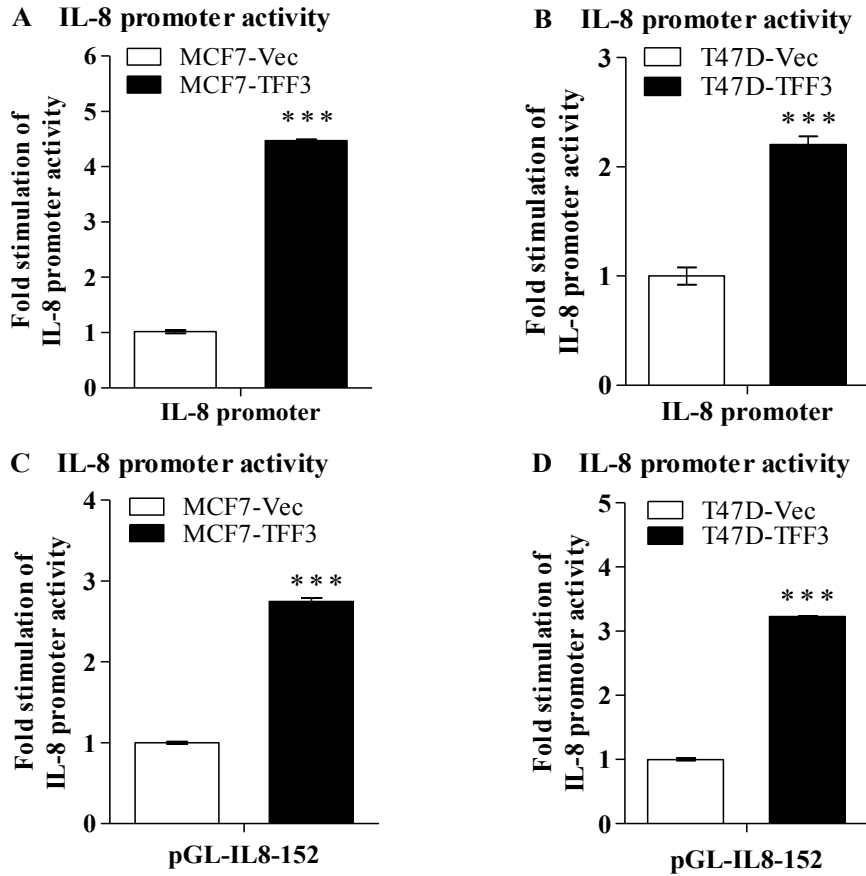


Figure 37: Forced expression of TFF3 in mammary carcinoma cells increased IL-8 promoter activity. A, IL-8 promoter activity (full length, -4800 to + 104 bp) in MCF-7 cells with forced expression of TFF3. MCF-7 cells with empty vector were used as control. B, IL-8 promoter activity in T47D cells with forced expression of TFF3. T47D cells with empty vector were used as control. C, IL-8 promoter activity in MCF7-Vec and MCF7-TFF3 transiently transfected with pGL-IL8-152 reporter (-152 to +44 bp). D, IL-8 promoter activity in T47D-Vec and T47D-TFF3 transiently transfected pGL-IL8-152 reporter. Reporter constructs consist of 5' flanking regions of the IL-8 gene were subcloned upstream of a luciferase reporter gene in the pGL3 basic vector. pGL-IL8-152 reporter construct encompassing nucleotides -152 to +44 of the IL-8 promoter, which was consist of NF-IL6, AP-1, NFκB binding sites. The TATA box, and the NF-IL6, NFκB and AP-1 binding sites are located at -13, -70, -80 and -120, respectively. Fold stimulation was measured by the ratio firefly luciferase of IL-8 reporter in MCF7-TFF3 and T47D-TFF3 to firefly luciferase of IL-8 reporter in MCF7-Vec and T47D-Vec. ***, $P < 0.001$.

3.2.11 Depletion of TFF3 in mammary carcinoma cells decreased IL-8 promoter activity

To determine if depletion of TFF3 by siRNA in mammary carcinoma cells decreased IL-8 expression, mammary carcinoma cells with depletion of TFF3 were transiently transfected with an IL-8 reporter vectors including IL-8 promoter (-1480 to +104 bp) or pGL-IL8-152 reporter vector, together with a pRL-CMV control reporter vector. MCF-7 and T47D cells with depletion of TFF3 and transiently transfected with a full length of IL-8 promoter (-1480 to +104 bp) exhibited significantly decreased IL-8 promoter activity by 3.4-fold or 1.7-fold respectively when compared with the respective control cells (Figure 38A-B). Additionally, MCF-7 and T47D cells with depletion of TFF3 and transiently transfected with a shorter IL-8 promoter, pGL-IL8-152 reporter vector, exhibited significantly decreased IL-8 promoter activity when compared with the respective control cells (Figure 38C-D). These data indicated that depletion of TFF3 in mammary carcinoma cells by siRNA abrogated IL-8 promoter activity and the transcription factors namely AP-1, NF-IL-6 and NF- κ B were necessary for TFF3-stimulated IL-8 promoter activity. Subsequently, depletion of TFF3 in MCF-7 and T47D cells decreased IL-8 mRNA (Figure 39A-B) and IL-8 protein secreted to the medium (Figure 39C-D) when compared with the respective control cells. Depletion of TFF3 by siRNA reduced IL-8 promoter activity and subsequently decreased the expression of IL-8 in mammary carcinoma cells.

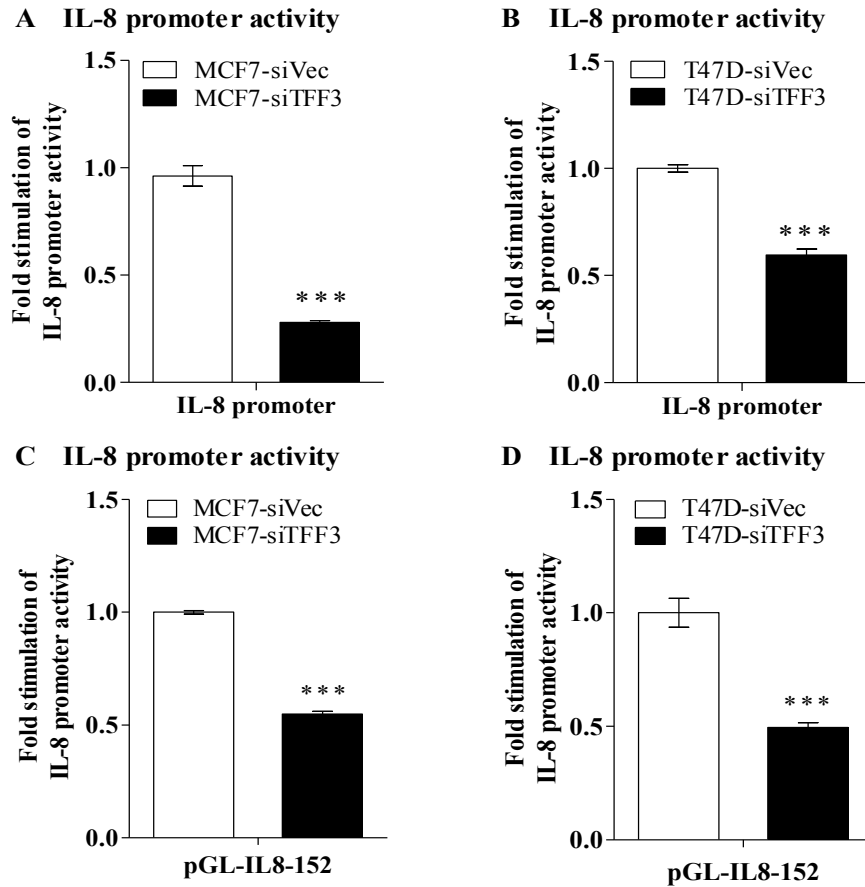


Figure 38: Depletion of TFF3 in mammary carcinoma cells decreased IL-8 promoter activity. A, IL-8 promoter reporter activity (full length, -4800 to + 104 bp) in MCF-7 cells with depletion of TFF3. MCF-7 cells with empty vector were used as control. B, IL-8 promoter reporter activity (full length, -4800 to + 104 bp) in T47D cells with depletion of TFF3. T47D cells with empty vector were used as control. C, IL-8 promoter activity in MCF7-Vec and MCF7-TFF3 transiently transfected with a shorter IL-8 promoter namely pGL-IL8-152 reporter. D, IL-8 promoter activity in T47D-Vec and T47D-TFF3 transiently transfected pGL-IL8-152 reporter. . ***, $P < 0.001$.

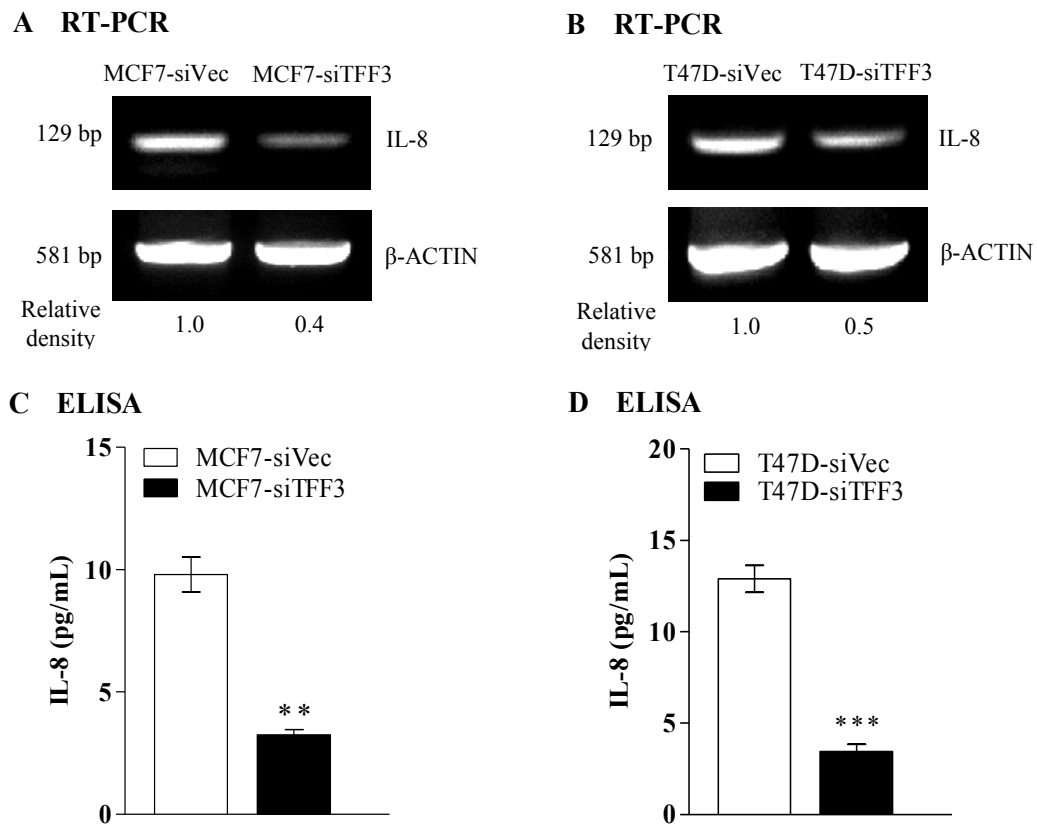


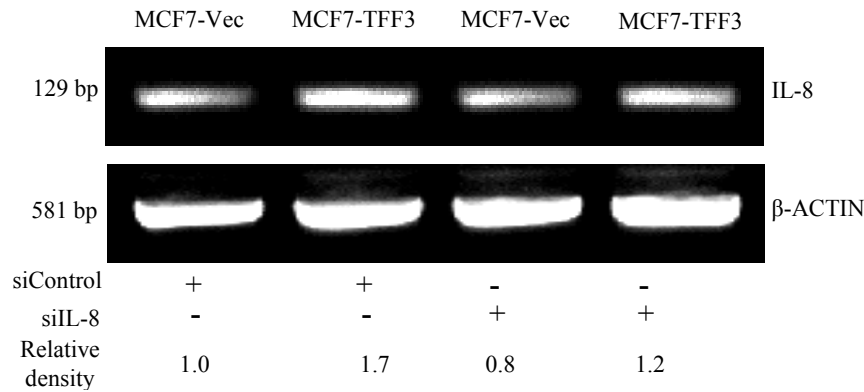
Figure 39: Depletion of TFF3 in mammary carcinoma cells decreased IL-8 expression. A, semi-quantitative RT-PCR analysis of IL-8 mRNA in MCF-7 cells with depletion of TFF3. MCF-7 cells with siRNA control vector were used as control. B, semi-quantitative RT-PCR analysis of IL-8 mRNA in T47D cells depletion of TFF3. T47D cells with siRNA control vector were used as control. C, ELISA analysis of IL-8 protein secreted to the medium by MCF-7 cells with depletion of TFF3. D, ELISA analysis of IL-8 protein secreted to the medium by T47D cells with depletion of TFF3. β-ACTIN was used as a loading control in semi-quantitative RT-PCR. **, $P < 0.01$, ***, $P < 0.001$.

3.2.12 Depletion of IL-8 by siRNA abrogated the stimulatory effect of TFF3 on HUVEC migration, invasion, and tubule formation *in vitro*

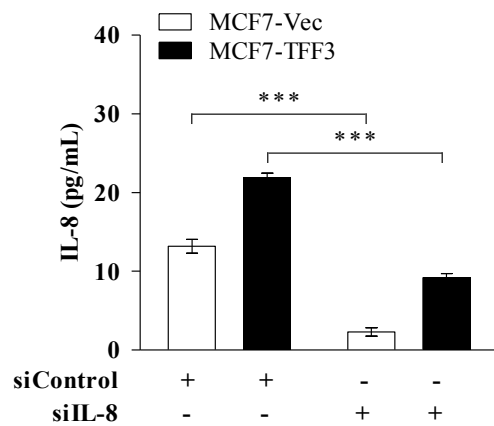
To determine if IL-8 mediated the stimulatory effect of TFF3 on the angiogenic behaviors of HUVEC, an IL-8 siRNA was employed to deplete the expression of IL-8 in MCF-7 cells with forced expression of TFF3. Hence, MCF-7 cells with forced expression of TFF3 were transiently transfected with an IL-8 siRNA (designated as siIL-8) or a scrambled control siRNA (designated as siControl). MCF-7 cells with forced expression of TFF3 and transiently transfected with IL-8 siRNA appeared to relatively decrease the expression of IL-8 mRNA (after 24 hours transfection) (Figure 40A). Semi-quantitative RT-PCR was not sensitive enough to detect the relative discrepancy of the IL-8 mRNA expression between MCF-7 cells with forced expression of TFF3 transiently transfected with IL-8 siRNA and those transiently transfected with scrambled control siRNA. Therefore, ELISA was used to quantify the concentration of IL-8 protein secreted to the medium. MCF-7 cells with forced expression of TFF3 and transiently transfected with IL-8 siRNA decreased IL-8 protein secreted to the medium (after 48 hours and 72 hours transfection) (Figure 40B-C) when compared with the respective siControl cells. IL-8 siRNA selectively depleted the expression of IL-8 in MCF-7 cells with forced expression of TFF3 and vector control cells. Subsequently, HUVEC were co-cultured with MCF7-Vec or MCF7-TFF3 with depletion of IL-8. Depletion of IL-8 in MCF7-Vec significantly decreased HUVEC migration by 42% (Figure 41A) and invasion by 42% (Figure 41B) when compared with the MCF7-Vec transiently transfected with control siRNA. Depletion of IL-8 in MCF7-TFF3 significantly decreased HUVEC migration by 74% (Figure 41A) and invasion by 65% (Figure 41B) when compared with MCF7-TFF3 transiently transfected with control siRNA, indicating that the depletion of IL-8 by siRNA abrogated the stimulatory effect of TFF3 on HUVEC migration and invasion. Furthermore, MCF7-Vec with depletion of IL-8 by siRNA significantly decreased tubule length by 43% (Figure 41C) and tubule number by 37% (Figure 41D) when compared with MCF7-Vec transiently transfected with control siRNA, indicating that depletion of IL-8 by

siRNA inhibited angiogenic effect of IL-8 on HUVEC tubule formation *in vitro*. Depletion of IL-8 in MCF7-TFF3 significantly decreased tubule length by 61% (Figure 41C) and tubule number by 58% (Figure 41D) when compared with MCF7-TFF3 transiently transfected with control siRNA, indicating that depletion of IL-8 by siRNA abrogated the stimulatory effects of TFF3 on HUVEC tubule formation *in vitro*. Depletion of IL-8 by siRNA in MCF-7 cells with forced expression of TFF3 significantly decreased tubules formed by the HUVEC in the Matrigel when compared with the control cells (Figure 41E). These data indicated that depletion of IL-8 by siRNA decreased the stimulatory effects of TFF3 on HUVEC tubule formation *in vitro*. Depletion of IL-8 in MCF-7 cells by siRNA abrogated the ability of TFF3 to stimulate angiogenic behaviors of HUVEC.

A RT-PCR



B ELISA: 48 hours post-transfection



C ELISA: 72 hours post-transfection

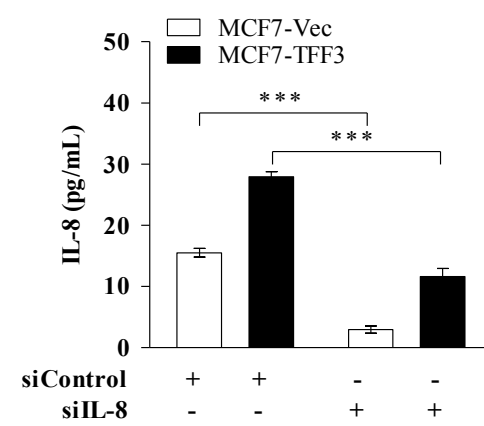
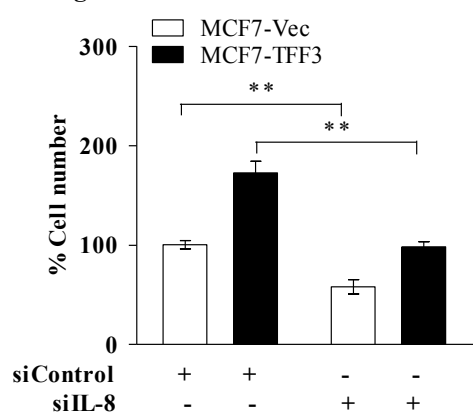
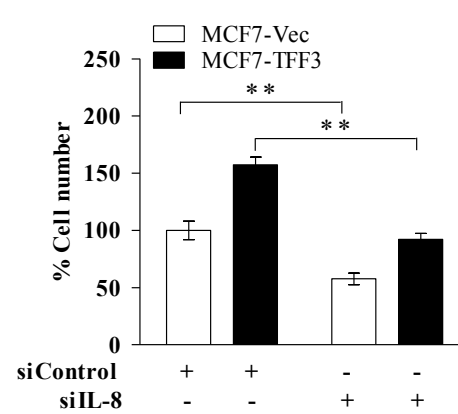


Figure 40: Depletion of IL-8 in mammary carcinoma cells with forced expression of TFF3 by siRNA decreased IL-8 expression. A, semi-quantitative RT-PCR of the expression of IL-8 mRNA in MCF-7 cells with forced expression of TFF3 transiently transfected with control siRNA or IL-8 siRNA after 24 hours transfection. Scrambled control siRNA was used as control. MCF7-Vec transiently transfected with scrambled control siRNA was used as baseline. B, ELISA analysis of IL-8 protein secreted to the medium by MCF-7 cells with forced expression of TFF3 transiently transfected with control siRNA or IL-8 siRNA after 48 hours transfection. C, ELISA analysis of IL-8 protein secreted to the medium by MCF-7 with forced expression of TFF3 transiently transfected with control siRNA or IL-8 siRNA after 72 hours transfection. β - ACTIN was used as a loading control in semi-quantitative RT-PCR. ***, $P < 0.001$ as compared with MCF7-Vec and MCF7-TFF3 transiently transfected with control siRNA.

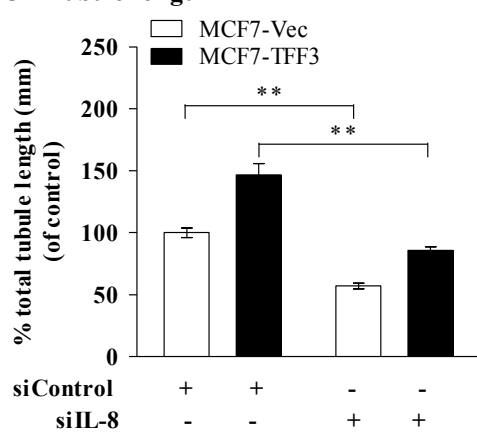
A Migration



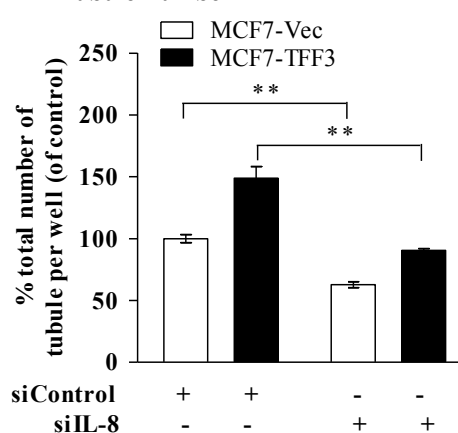
B Invasion



C Tubule length



D Tubule number



E Tubule formation

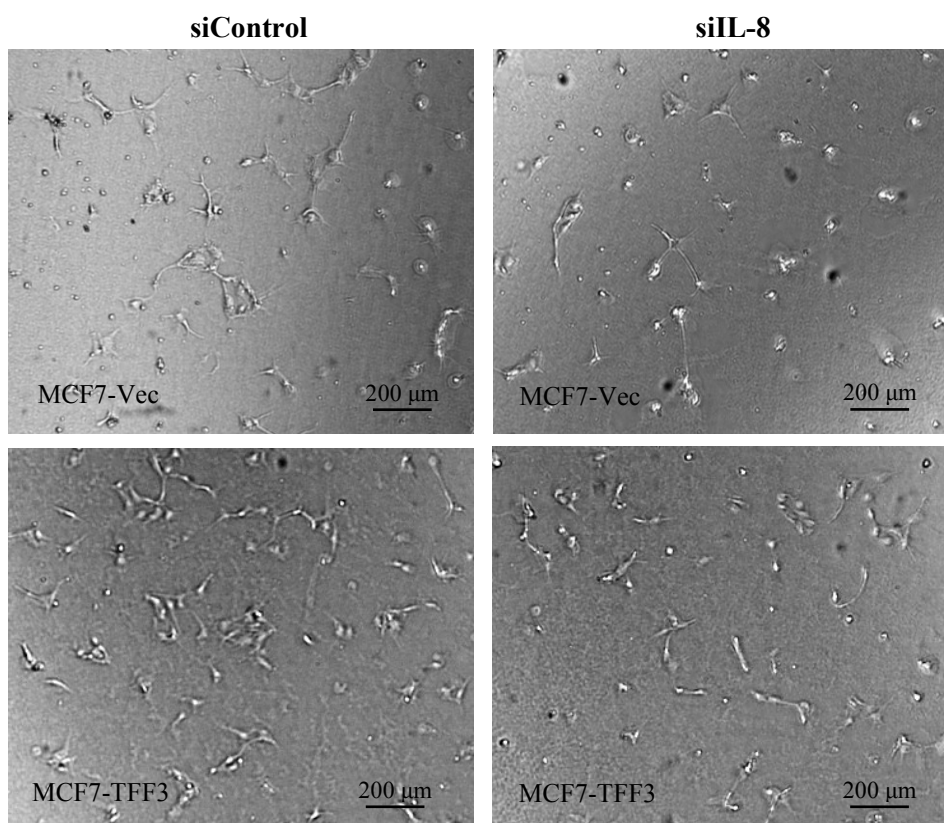


Figure 41: Depletion of IL-8 in mammary carcinoma cells by siRNA abrogated stimulatory effect of TFF3 on HUVEC migration, invasion, and tubule formation *in vitro*. A, HUVEC migration after 24 hours co-culture with MCF-7 cells with forced expression of TFF3 transiently transfected with control siRNA or IL-8 siRNA in serum-free conditions. Scrambled control siRNA was used as control. MCF7-Vec transiently transfected with scrambled control siRNA was used as baseline. B, HUVEC invasion after 24 hours co-culture with MCF-7 cells with forced expression of TFF3 transiently transfected with control siRNA or IL-8 siRNA in serum-free conditions. C and D, HUVEC tubule formation *in vitro* on Matrigel after 12 hours co-culture with MCF-7 cells with forced expression of TFF3 transiently transfected with control siRNA or IL-8 siRNA in serum-free conditions for 12 hours incubation. Total tubule length (C) and tubule number (D) was assessed using ImageJ analysis software. E, representative light microscopy images of HUVEC tubule formation *in vitro* in the Matrigel after 12 hours co-culture of with MCF7-Vec and MCF7-TFF3 transiently transfected with control siRNA or IL-8 siRNA. The light microscopy images were taken at $\times 40$ magnification. **, $P < 0.01$ as compared with MCF7-Vec and MCF7-TFF3 transiently transfected with control siRNA; scale bar, 200 μm .

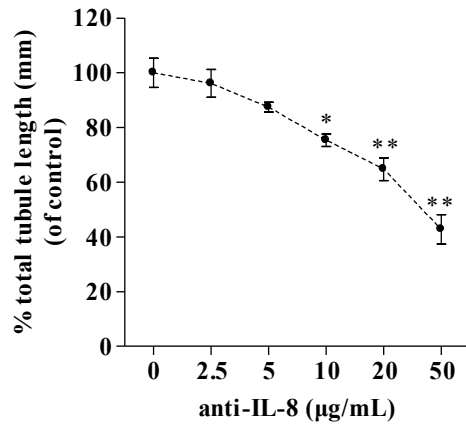
3.2.13 Blocking IL-8 in mammary carcinoma cells by anti-IL-8 monoclonal antibody inhibited the stimulatory effect of TFF3 on HUVEC tubule formation *in vitro*

The development of humanized monoclonal antibodies against IL-8 has been exploited to inhibit the tumor-promoting effect of IL-8 in melanoma and bladder xenograft models (Huang *et al.*, 2002, Mian *et al.*, 2003). Humanized anti-IL-8 monoclonal antibodies (e.g., ABX-IL8) bind to IL-8 and prevent it from binding to its receptors (Yang *et al.*, 1999, Huang *et al.*, 2002, Mian *et al.*, 2003). Administration of anti-IL-8 antibodies suppress IL-8 signaling on tumor progression and development (Huang *et al.*, 2002). Accordingly, an anti-IL-8 monoclonal antibody was utilized for blocking IL-8 in MCF-7 cells with forced expression of TFF3 and vector control cells. To initially determine the effect of blocking IL-8 in control MCF7-Vec on the IL-8-mediated HUVEC tubule formation *in vitro*, HUVEC were co-cultured with MCF7-Vec treated with different concentration of anti-IL-8 monoclonal antibody (2.5, 5.0, 10.0, 20.0, 50.0 $\mu\text{g/mL}$) or IgG control (50.0 $\mu\text{g/mL}$). Blocking IL-8 in MCF7-Vec by different concentration of anti-IL-8 monoclonal antibody decreased tubule length in a concentration-dependent manner, with 57% reduction of HUVEC tubule formation *in vitro* at 50 $\mu\text{g/mL}$ anti-IL-8 monoclonal antibody (Figure 42A). These data indicated that

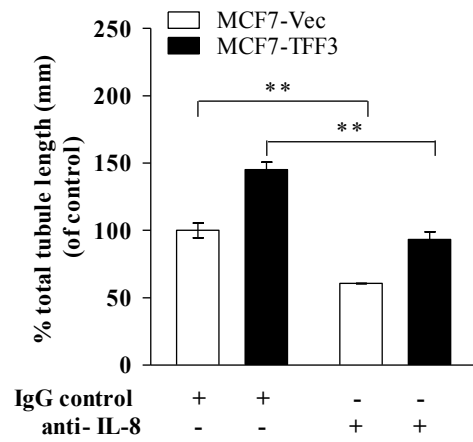
blocking of IL-8 in control MCF7-Vec by anti-IL-8 monoclonal antibody decreased HUVEC tubule formation *in vitro*.

To determine if blocking of IL-8 by anti-IL-8 monoclonal antibody inhibited the stimulatory effect of TFF3 on HUVEC tubule formation *in vitro*, HUVEC were co-cultured with MCF7-Vec and MCF7-TFF3 treated with 50 µg/mL of anti-IL-8 monoclonal antibody or IgG control. Blocking of IL-8 in MCF7-Vec by anti-IL-8 monoclonal antibody significantly decreased tubule length by 39% (Figure 42B) and tubule number by 40% (Figure 42C) when compared with MCF7-Vec treated with IgG control, indicating that inhibition of IL-8 in MCF7-Vec by anti-IL-8 monoclonal antibody attenuated IL-8-mediated angiogenesis *in vitro*. Blocking of IL-8 in MCF7-TFF3 by anti-IL-8 monoclonal antibody significantly decreased tubule length by 52% (Figure 42B) and tubule number by 49% (Figure 42C) when compared with MCF7-TFF3 treated with IgG control, indicating that blocking of IL-8 in MCF7-TFF3 cells by anti-IL-8 monoclonal antibody inhibited the stimulatory effect of TFF3 in angiogenesis *in vitro*. Blocking of IL-8 in MCF7-Vec or MCF7-TFF3 by anti-IL-8 monoclonal antibody significantly decreased tubules formed by HUVEC in the Matrigel when compared with the respective cells treated with IgG control (Figure 42D). Depletion of IL-8 in MCF-7 cells by anti-IL-8 monoclonal antibody inhibited the ability of TFF3 to stimulate angiogenic behaviors of HUVEC mediated by IL-8.

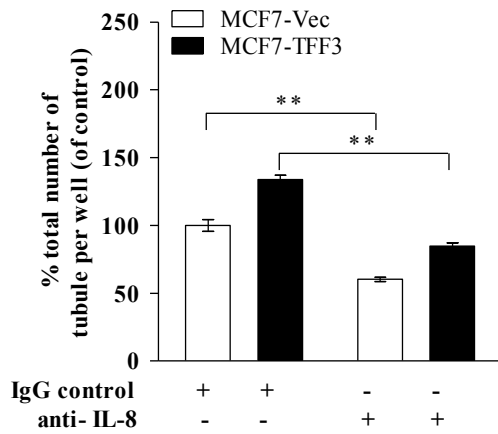
A Tubule length



B Tubule length



C Tubule number



D Tubule formation

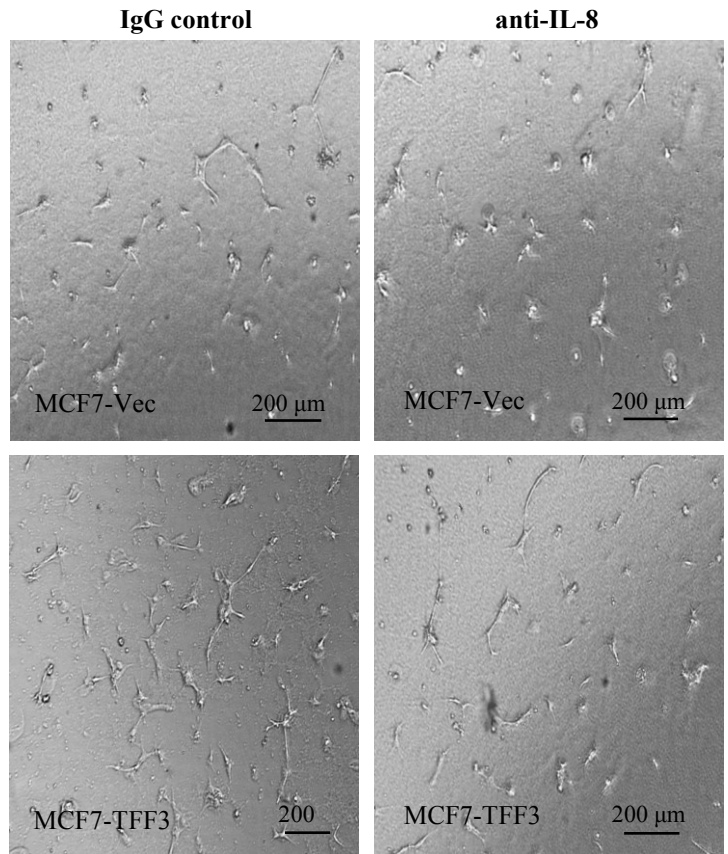


Figure 42: Blocking IL-8 in mammary carcinoma cells by anti-IL-8 monoclonal antibody inhibited the ability of TFF3 on stimulation of HUVEC tubule formation *in vitro*. A, HUVEC tubule formation *in vitro* in the Matrigel after 12 hours co-culture with MCF7-Vec treated with different concentration of anti-IL-8 monoclonal antibody (2.5, 5.0, 10.0, 20.0, 50 $\mu\text{g/mL}$) or IgG control in serum-free conditions. IgG was used as control. Total tubule length was assessed after 12 hours incubation. B and C, HUVEC tubule formation *in vitro* on Matrigel after 12 hours co-culture with control vector cells or MCF-7 cells with forced expression of TFF3 treated with IgG control and 50 $\mu\text{g/mL}$ of anti-IL-8 monoclonal antibody in serum-free conditions. Total tubule length (B) and tubule number (C) was assessed using ImageJ analysis software. D, representative light microscopy images of HUVEC tubule formation *in vitro* in the Matrigel after 12 hours co-culture with MCF7-Vec or MCF7-TFF3 treated with IgG control and 50 $\mu\text{g/mL}$ anti IL-8 monoclonal antibody. IgG control was used as control. MCF7-Vec treated with IgG control was used as baseline. The light microscopy images were taken at x40 magnification. *, $P < 0.05$; **, $P < 0.01$ as compared to MCF7-Vec and MCF7-TFF3 treated with IgG control; scale bar, 200 μm .

3.2.14 Blocking CXCR2 in HUVEC inhibited IL-8 mediated stimulatory effect of TFF3 on HUVEC tubule formation *in vitro*

IL-8 receptors CXCR1 and CXCR2 are highly expressed in cancer and endothelial cells to mediate the angiogenic function of IL-8 in tumor angiogenesis (Holmes *et al.*, 1991, Cerretti *et al.*, 1993). Neutralizing antibody to IL-8, CXCR1 or CXCR2 has been reported to inhibit endothelial cell proliferation and capillary tube formation (Li *et al.*, 2005). To determine whether blocking CXCR2 in HUVEC inhibited tubule formation *in vitro*, parental HUVEC were treated with different concentration of anti-CXCR2 monoclonal antibody. HUVEC tubule formation *in vitro* was inhibited by anti-CXCR2 monoclonal antibody in a concentration-dependent manner, with 44% reduction of tubule length at 20 $\mu\text{g/mL}$ anti-CXCR2 monoclonal antibody (Figure 43A). These data indicated that anti-CXCR2 monoclonal antibody inhibited HUVEC tubule formation *in vitro* in a concentration-dependent manner.

To determine whether the effect of TFF3 on stimulation of HUVEC tubule formation *in vitro* was mediated by IL-8 through CXCR1 or CXCR2 receptor, MCF7-Vec and MCF7-TFF3 co-cultured with HUVEC were treated with 20 $\mu\text{g/mL}$ anti-CXCR2 or anti-CXCR1 monoclonal antibody respectively. Co-culturing MCF7-Vec and MCF7-TFF3 with HUVEC

treated with anti-CXCR1 monoclonal antibody exhibited similar or slight changes in tubule length and tubule number when compared with the respective cells co-cultured with HUVEC treated with IgG control (Figure 44A-C). Anti-CXCR1 monoclonal antibody presumably was not able to affect the ability of TFF3 on stimulation of HUVEC tubule formation *in vitro*. However, co-culturing MCF7-Vec with HUVEC treated with anti-CXCR2 monoclonal antibody decreased tubule length by 41% (Figure 43B) and tubule number by 47% (Figure 43C) when compared with HUVEC treated with IgG control. Co-culturing MCF7-TFF3 with HUVEC treated with anti-CXCR2 monoclonal antibody significantly decreased tubule length by 66% (Figure 43B) and tubule number by 58% (Figure 43C) when compared with HUVEC treated with IgG control. Co-culturing MCF7-Vec and MCF7-TFF3 with HUVEC treated with anti-CXCR2 monoclonal antibody decreased tubules in the Matrigel when compared with MCF7-Vec and MCF7-TFF3 co-cultured with HUVEC treated with IgG control (Figure 43D). These observations indicated that blocking of CXCR2 in HUVEC by anti-CXCR2 monoclonal antibody inhibited the effect of TFF3 on the stimulation of angiogenic behaviors of HUVEC mediated by IL-8 through CXCR2 receptor. It is also possible that the anti-CXCR2 monoclonal antibody is disrupting IL-8-independent events because CXCR2 binds to IL-8 and other chemokines.

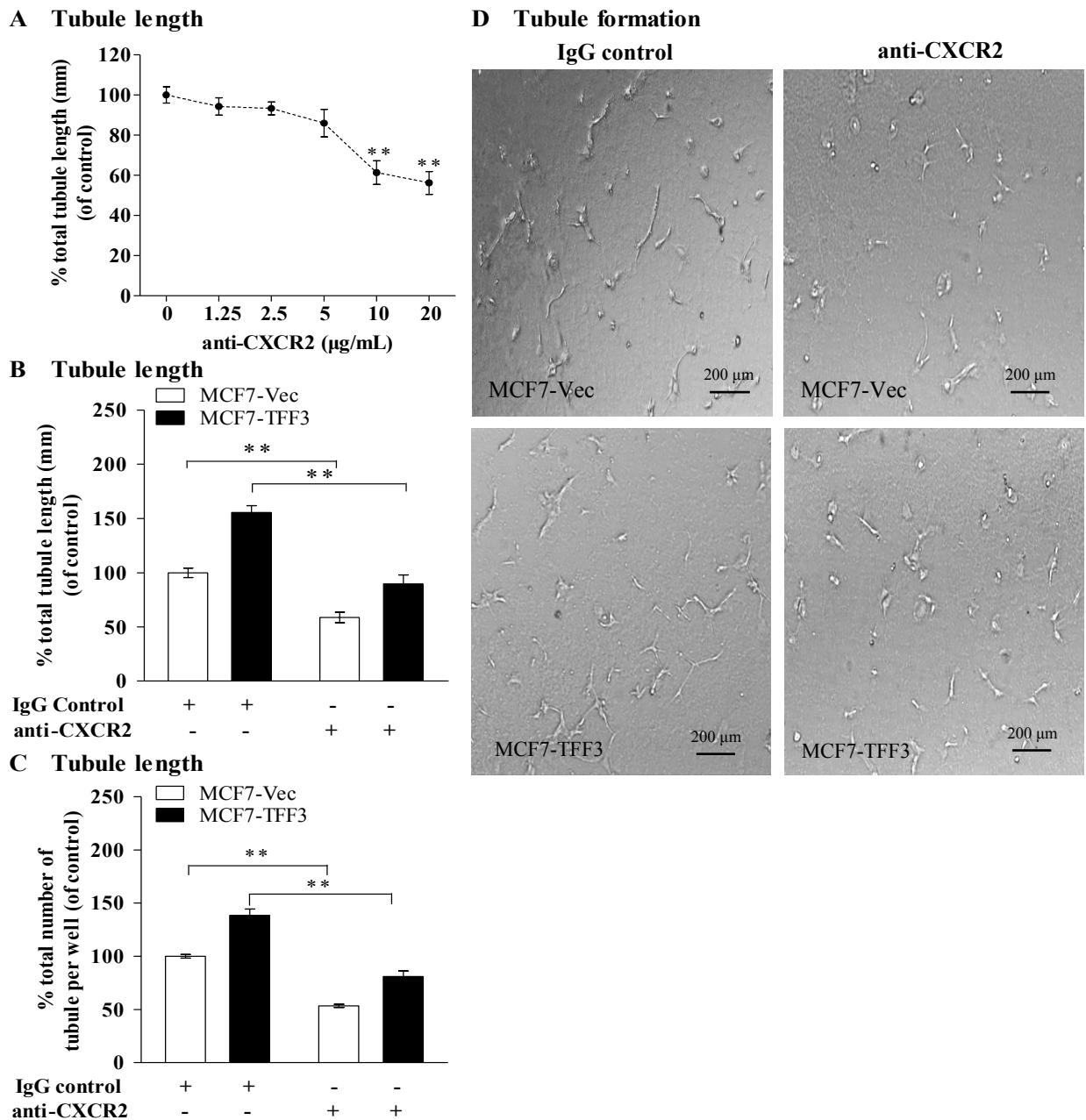


Figure 43: Blocking of CXCR2 in HUVEC by anti-CXCR2 monoclonal antibody inhibited IL-8 mediated stimulatory effect of TFF3 on HUVEC tubule formation *in vitro*. A, HUVEC tubule formation *in vitro*, in which HUVEC treated with different concentration of anti-CXCR2 monoclonal antibody (1.25, 2.5, 5.0, 10.0, 20 µg/mL) or IgG control. IgG was used as control. MCF7-Vec co-cultured with HUVEC treated with IgG control was used as baseline. Total tubule length was assessed after 12 hours incubation. B and C, HUVEC tubule formation *in vitro*, in which control vector cells or MCF-7 cells with forced expression of TFF3 co-cultured with HUVEC treated with IgG control and 20 µg/mL of anti-CXCR2 monoclonal antibody. Total tubule length (B) and tubule number (C) was assessed by ImageJ analysis software. D, representative light microscopy images of HUVEC tubule formation *in vitro*, in which MCF7-Vec and MCF7-TFF3 co-cultured with HUVEC treated with IgG control and 20 µg/mL of anti-CXCR2 monoclonal antibody. IgG was used as control. MCF7-Vec co-cultured with HUVEC treated with IgG control was used as baseline. The light microscopy images were taken at $\times 40$ magnification. **, $P < 0.01$ as compared to HUVEC treated with IgG control; scale bar, 200 µm.

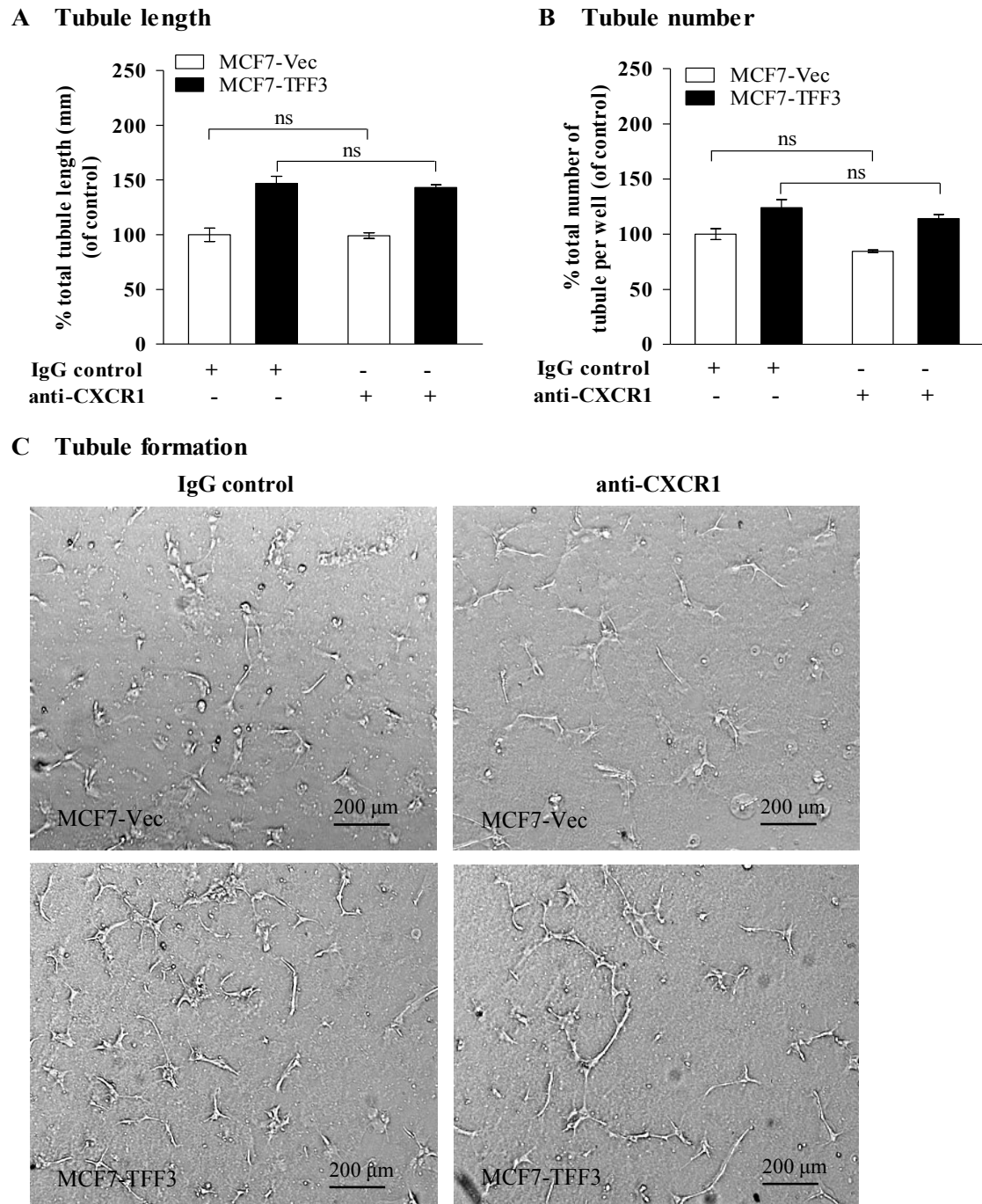


Figure 44: Blocking of CXCR1 in HUVEC by anti-CXCR1 monoclonal antibody did not affect IL-8 mediated stimulatory effect of TFF3 on HUVEC tubule formation *in vitro*. A and B, HUVEC tubule formation *in vitro*, in which control vector cells or MCF-7 cell with forced expression of TFF3 co-cultured with HUVEC treated with IgG control and 20 μ g/mL anti-CXCR1 monoclonal antibody. Total tubule length (A) and tubule number (B) was assessed by ImageJ analysis software. C, representative light microscopy images of HUVEC tubule formation *in vitro*, in which MCF7-Vec and MCF7-TFF3 co-cultured with HUVEC treated with IgG control or 20 μ g/mL of anti-CXCR1 monoclonal antibody. IgG was used as control. MCF7-Vec co-cultured with HUVEC treated with IgG control was used as baseline. The light microscopy images were taken at $\times 40$ magnification. n.s indicated not significant, as compared to HUVEC treated with IgG control; scale bar, 200 μ m.

3.2.15 Forced expression of TFF3 in mammary carcinoma cells promoted activation of STAT3 and subsequently partially increased IL-8 expression

In addition to the three main transcription factors NF- κ B, NF-IL-6, and AP-1, TFF3 may be stimulated other transcription factors for regulation of IL-8 expression. STAT3 regulated IL-8 expression presumably through direct binding to its consensus binding site at the IL-8 promoter region (Oka *et al.*, 2010). To determine if TFF3 stimulated activation of STAT3 (tyrosine 705 phosphorylation) in MCF-7 cells, the expression of total STAT3 and Y705 phosphorylated STAT3 protein (STAT3 α and STAT3 β isoforms) in MCF-7 cells with forced expression of TFF3 were analyzed by Western blot analysis. When compared with control MCF7-Vec, forced expression of TFF3 in MCF-7 cells increased Y705 phosphorylated STAT3 proteins (STAT3 α and STAT3 β isoforms) and exhibited relatively similar level of total STAT3 protein (Figure 45A), indicating that TFF3 increased Y705 phosphorylated STAT3 protein and presumably not affected the total STAT3 protein expression.

To determine if TFF3 stimulated activation of STAT3 in MCF-7 cells and involved in the regulate IL-8 expression, STAT3 siRNA was employed to deplete STAT3 and therefore decreased STAT3 activity in mammary carcinoma cells. MCF-7 cells with forced expression of TFF3 were transiently transfected with a pcDNA containing STAT3 siRNA (siSTAT3) or pcDNA vector containing control siRNA (siControl). The expressions of total STAT3 and Y705 phosphorylated STAT3 in MCF7-Vec and MCF7-TFF3 with depletion of STAT3 were analyzed by Western blot analysis. Depletion of STAT3 in MCF-7 cells with forced expression of TFF3 decreased total STAT3 protein and Y705 phosphorylated STAT3 protein (Figure 45B) when compared with the respective cells transiently transfected with control siRNA. Subsequently, MCF7-Vec and MCF7-TFF3 with depletion of STAT3 were transiently transfected with a full length of IL-8 promoter reporter vector (-1480 to + 104 bp) and a pRL-CMV control reporter vector. Depletion of STAT3 by siRNA in MCF7-Vec and MCF7-TFF3 resulted in a small but consistently decreased of IL-8 promoter activity when

compared with the respective siControl cells (Figure 45C), indicating that STAT3 siRNA partially inhibited the effect of TFF3 on stimulation of IL-8 promoter activity. Additionally, depletion of STAT3 by siRNA partially abrogated the ability of TFF3 to regulate the expression of IL-8 and resulted in a small but consistently decreased expression of IL-8 mRNA (Figure 45D) and IL-8 protein secreted to the medium (Figure 45E) when compared with the respective siControl cells. These observations indicated that depletion of STAT3 by siRNA in MCF-7 cells partially reduced IL-8 promoter activity and subsequently led to a small decreased of IL-8 expression.

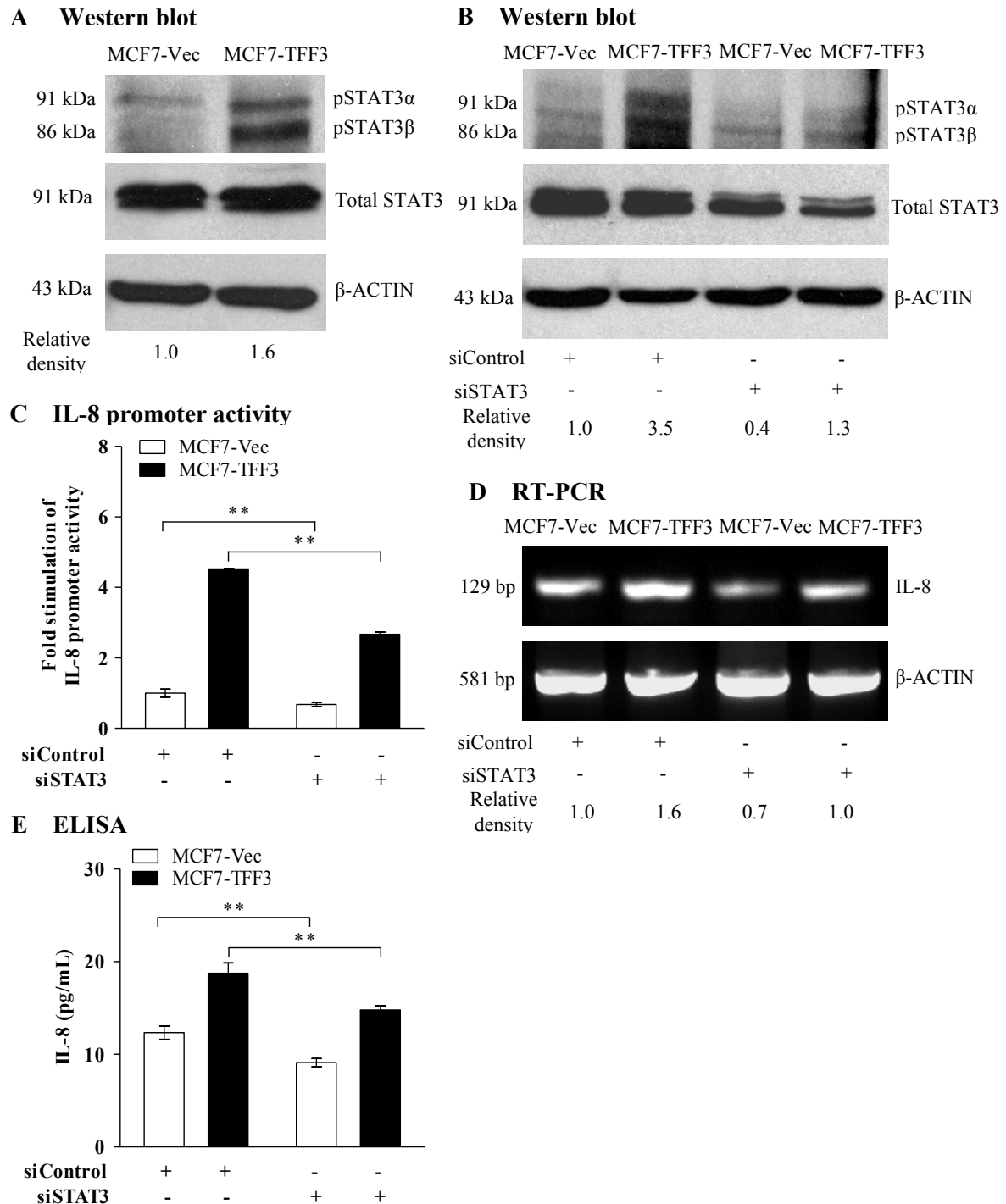


Figure 45: Forced expression of TFF3 in mammary carcinoma cells promoted the activation of STAT3 and subsequently partially increased IL-8 expression. A, Western blot analysis of total STAT3 protein and Y705 phosphorylated STAT3 (pSTAT3) in MCF-7 cells with forced expression of TFF3. B, Western blot analysis of total STAT3 and Y705 phosphorylated STAT3 protein in MCF7-Vec and MCF7-TFF3 transiently transfected with pcDNA vector containing STAT3 siRNA or control siRNA. C, IL-8 promoter activity in MCF7-Vec and MCF7-TFF3 with depletion of STAT3 transiently transfected with an IL-8 promoter reporter vector and a pRL-CMV control reporter vector. Scrambled control siRNA was used as control. MCF7-Vec transiently transfected with scrambled control siRNA was used as baseline. D, semi-quantitative analysis of IL-8 mRNA expression in MCF-7 cells with

forced expression of TFF3 transiently transfected with pcDNA vector containing STAT3 siRNA or control siRNA. E, ELISA analysis of IL-8 protein secreted to the medium by MCF7-Vec and MCF7-TFF3 transiently transfected with pcDNA vector containing STAT3 siRNA or control siRNA. β -ACTIN was used as a loading control in semi-quantitative RT-PCR and Western blot analysis. **, $P < 0.01$ as compared MCF7-Vec or MCF7-TFF3 transiently transfected with control siRNA.

3.2.16 Depletion of STAT3 by siRNA partially abrogated stimulatory effect of TFF3 on HUVEC migration, invasion, and tubule formation *in vitro*

To determine if STAT3 mediated TFF3 enhancement of angiogenic behaviors of endothelial cells, HUVEC were co-culture with MCF7-Vec and MCF7-TFF3 with depletion of STAT3. Depletion of STAT3 by siRNA in MCF7-Vec partially decreased HUVEC migration by 36% (Figure 46A) and invasion by 31% (Figure 46B) when compared with MCF7-Vec transiently transfected with control siRNA. Depleted expression of STAT3 in MCF7-TFF3 partially decreased HUVEC migration by 47% (Figure 46A) and invasion by 58% (Figure 46B) when compared with MCF7-TFF3 transiently transfected with control siRNA. These observations indicated that depletion of STAT3 by siRNA partially abrogated the ability of TFF3 to stimulate HUVEC migration and invasion.

Furthermore, depletion of STAT3 in MCF7-Vec significantly decreased tubule length by 32% (Figure 46C) and tubule number by 31% (Figure 46D) when compared with MCF7-Vec transiently transfected with control siRNA. Depletion of STAT3 in MCF7-TFF3 significantly decreased tubule length by 46% (Figure 46C) and tubule number by 58% (Figure 46D) when compared with MCF7-TFF3 transiently transfected with control siRNA. Depleted expression of STAT3 by siRNA in MCF7-Vec and MCF-TFF3 significantly decreased tubules formed by the HUVEC when compared with the respective siControl cells (Figure 46E). These observations indicated that depletion of STAT3 by siRNA partially abrogated the ability of TFF3 on stimulation of HUVEC tubule formation *in vitro*.

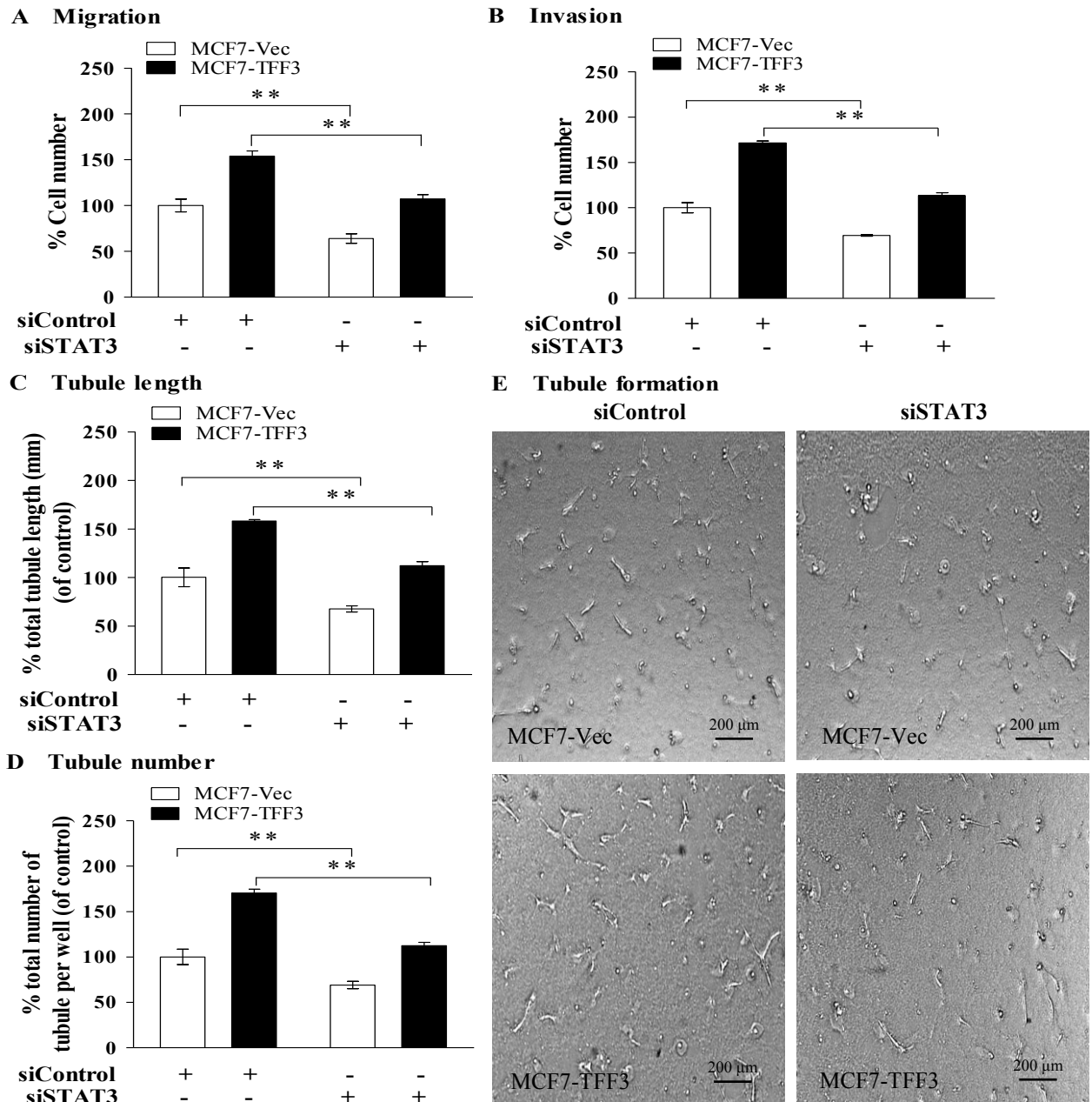


Figure 46: Depletion of STAT3 in mammary carcinoma cells by siRNA partially abrogated stimulatory effect of TFF3 on HUVEC migration, invasion, and tubule formation *in vitro*. A, HUVEC migration after 24 hours co-culture with MCF-7 cells with forced expression of TFF3 transiently transfected with STAT3 siRNA. Scrambled control siRNA was used as control. MCF7-Vec transiently transfected with scrambled control siRNA was used as baseline. B, HUVEC invasion after 24 hours co-culture with MCF-7 cells with forced expression of TFF3 transiently transfected with control siRNA or STAT3 siRNA. C and D, HUVEC tubule formation *in vitro* in the Matrigel after 12 hours co-culture with MCF-7 cells with forced expression of TFF3 transiently transfected with control siRNA or STAT3 siRNA in serum-free conditions. Total tubule length (C) and tubule number (D) was assessed. E, representative light microscopy images of HUVEC tubule formation *in vitro* in the Matrigel after 12 hours co-culture of with MCF7-Vec and MCF7-TFF3 transiently transfected with control siRNA or STAT3 siRNA. The light microscopy images were taken at $\times 40$ magnification. **, $P < 0.01$ as compared to MCF7-Vec or MCF7-TFF3 transiently transfected with control siRNA; scale bar, 200 μm .

3.3 Discussion

3.3.1 Forced expression of TFF3 in mammary carcinoma cells promoted de novo angiogenesis

TFF3 has been reported increased its expression in mammary carcinoma and the expression of TFF3 is positively associated with metastasis and poor survival outcome of patients with ER+ mammary carcinoma (Smid *et al.*, 2006, Kannan *et al.*, 2010, Pandey *et al.*, 2014). Increased TFF3 expression in mammary carcinoma cells promotes tumor growth and metastatic progression by promoting cell survival and invasion (Kannan *et al.*, 2010, Ahmed *et al.*, 2012, Pandey *et al.*, 2014). It is known that TFF3 is an estrogen-responsive gene and its expression is associated with the ER status in human mammary carcinoma (May and Westley, 1997a, Gruvberger *et al.*, 2001). However, there is a subset of ER- mammary carcinoma cells that express high levels of TFF3 (Doane *et al.*, 2006). Herein, I have demonstrated that ER+ mammary carcinoma cells endogenously expressed TFF3 protein. Both MCF-7 and T47D cells expressed moderate levels of TFF3 and were utilized as mammary adenocarcinoma cell models. HUVEC was used as an *in vitro* model to investigate the stimulatory effect of TFF3 secreted from mammary carcinoma cells on the angiogenic behaviors of endothelial cells. TFF3 secreted from mammary carcinoma cells promoted HUVEC monolayer proliferation, cell cycle progression, survival, migration, invasion and tubule formation *in vitro*. Depletion of TFF3 in mammary carcinoma cells by siRNA diminished angiogenic behaviors of HUVEC.

During neovascularization, endothelial cells invade to avascular environments to generate vasculature in the tumor (Hanahan and Folkman, 1996). The survival of endothelial cells is one of the major factors for maintaining the stability of vascularity in the growing tumor (Nor *et al.*, 1999). It has been reported that TFF3 decreased apoptotic cell death of MCF-7 cells by approximately 10% in serum free conditions (Kannan *et al.*, 2010). I have demonstrated that TFF3 secreted from MCF7 cells decreased HUVEC apoptotic cell death by 61% in 10%FBS condition and 52% in serum free conditions. Similarly, Artemin secreted from mammary carcinoma cells decreased apoptotic cell death of endothelial cells in serum

deprived condition by 20% (Banerjee *et al.*, 2012). It is possible that the survival of endothelial cells was not affected by the supplemental function of serum but is dependent on the pro-survival effect of TFF3. I have demonstrated that TFF3 secreted by mammary carcinoma cells with forced expression of TFF3 promoted HUVEC proliferation and survival. TFF3 may also a pro-survival factor for endothelial cells. It has previously been reported that TFF3 is a pro-survival factor for cancer cells (Chen *et al.*, 2000, Taupin *et al.*, 2000b, Regalo *et al.*, 2005, Kannan *et al.*, 2010) and induced resistance to serum deprivation and drug-induced apoptosis in colon carcinoma cells (Emami *et al.*, 2004). Forced expression of TFF3 increased Bcl-2 (Kannan *et al.*, 2010), which is an anti-apoptotic protein (Yip and Reed, 2008) and decreased Bax, which is a pro-apoptotic Bcl-2-family proteins (Yip and Reed, 2008, Czabotar *et al.*, 2009). Increased the expression of Bcl-2 mediated TFF3-stimulated resistance to serum deprivation and doxorubicin-induced apoptosis in mammary carcinoma cells (Kannan *et al.*, 2010). TFF3 appears to be linked with multiple survival pathways including mitogen-activated protein kinase (MAPK) (Taupin *et al.*, 1999), phosphatidylinositol-3-kinase-Akt (PI3K-Akt) (Kinoshita *et al.*, 2000b, Taupin *et al.*, 2000b), STAT3 (Rivat *et al.*, 2005) and nuclear factor kappa B (NF- κ B) (Chen *et al.*, 2000). Enhanced Bcl2 expression is probably a consequence of activation of survival pathways, resulting from increased TFF3 expression (Kannan *et al.*, 2010). Additionally, I have demonstrated that forced expression of TFF3 in mammary carcinoma cells promoted HUVEC migration and invasion. TFF peptides induced cellular invasion of kidney and colonic carcinoma cells through autocrine loops (Emami *et al.*, 2001). TFF3 also promoted colon carcinoma cell migration through repression of E-cadherin-catenin complex formation and loss of cell adhesion (Emami *et al.*, 2004).

De novo angiogenesis is a fundamental requirement for tumor growth and metastasis of mammary carcinoma. High microvessel density has been associated with metastasis and poor survival in node-negative mammary carcinoma (Schneider and Miller, 2005, Fox *et al.*, 2007, Ran *et al.*, 2010). TFF3 has been implicated in tumor progression by promoting cell scattering and cellular invasion (Rodrigues *et al.*, 2003b). Increased the expression of TFF3

was positively correlated with microvessel density as evaluated by CD31 and CD34 of endothelial markers in gastric carcinoma (Dhar *et al.*, 2005) and mammary carcinoma (Ahmed *et al.*, 2012). Concordantly, I have demonstrated that TFF3 secreted from mammary carcinoma cells promoted HUVEC tubule formation *in vitro*. Hence, TFF3 secreted from mammary carcinoma cells stimulated angiogenic behaviors of HUVEC to promote *in vitro* angiogenesis. In xenograft models, TFF3 enhanced microvessel density (increased areas of CD31 and CD34 labeled cells) in the tumors produced by MCF-7 cells and suggesting that TFF3 promoted *in vivo* angiogenesis. These observations further supported that TFF3 promotes *de novo* angiogenesis in mammary carcinoma and therefore TFF3 is as a promoter of angiogenesis.

3.3.2 The mechanism by which TFF3 promoted *de novo* angiogenesis in mammary carcinoma cells

(i) IL-8 mediated angiogenic behaviors of endothelial cells stimulated by TFF3

Herein, I have demonstrated that TFF3 may not enhance VEGF-A expression in mammary carcinoma cells, suggesting that VEGF-A probably may not involve in modulation of TFF3 to stimulate angiogenic behaviors of HUVEC. TFF3 promoted *de novo* angiogenesis in mammary carcinoma is probably independent of VEGF-A signaling. These observations were unexpected because several reports have suggested that the angiogenic responses of VEGF-A are mediated by VEGFR2 receptor and it also stimulated activation of COX-2 or EGF-R tyrosine kinase to exert its angiogenic functions controlled by TFF peptides (Rodrigues *et al.*, 2003). It is well-known that VEGF-A plays a dominant role in tumor angiogenesis and is a potent angiogenic cytokine. VEGF-A promotes proliferation, migration, and survival of endothelial cells (Ferrara *et al.*, 2003, Ferrara, 2005). Increased VEGF-A expression is associated with tumor angiogenesis and poor prognosis of patient with breast cancer (Schneider and Miller, 2005). TFF peptides are not acting through VEGF-A/VEGFR signaling pathway because VEGFR2 tyrosine kinase inhibitor was not effectively attenuated

invasion of colon cancer cells stimulated by TFF3 (Rivat *et al.*, 2005). Conversely, depletion of STAT3 by siRNA abrogated cellular invasion promoted by TFF3 and VEGF-A, suggesting that the autocrine self-activation of TFF3 and VEGF-A in colon cancer cells are dependent on STAT3 signal transduction pathway (Rivat *et al.*, 2005). Concordantly, TFF3 stimulated phosphorylation of c-Src and subsequently increased STAT3 activity which led to down-regulation of E-cadherin for promoting invasion and metastasis of mammary carcinoma (Pandey *et al.*, 2014).

Herein, I have demonstrated that forced expression of TFF3 in mammary carcinoma cells increased IL-8 promoter activity and subsequently enhanced IL-8 expression. In xenograft model, mammary carcinoma cells with forced expression of TFF3 produced tumor with increased IL-8 protein expression. Forced expression of TFF3 in mammary carcinoma cells increased IL-8 expression, which in turn mediated the stimulatory effect of TFF3 in promoting *de novo* angiogenesis of mammary carcinoma. It has been reported that chemokine and its cognate receptors play an important role in facilitating invasion, angiogenesis, and metastasis of cancer cells (Richmond *et al.*, 2009, Singh *et al.*, 2010). IL-8 directly promoted angiogenesis via stimulation of endothelial cell proliferation, migration, survival and tubule formation (Koch *et al.*, 1992, Hu *et al.*, 1993, Heidemann *et al.*, 2003, Snyder *et al.*, 2004, Ning *et al.*, 2010). Increased IL-8 expression is associated with enhancing invasion and angiogenesis in mammary carcinoma (Lin *et al.*, 2004). Furthermore, IL-8 has been suggested as a metastatic factor in mammary carcinoma to regulate angiogenesis, tumor growth, and dissemination of cancer cells (Murdoch *et al.*, 1999, Salcedo *et al.*, 2000b). An *in vivo* study showed that the basal level of IL-8 expression is substantially higher in the estrogen-independent mammary carcinoma cell lines (e.g. MDA-MB-231) when compared with the estrogen-dependent mammary carcinoma cell lines (e.g. MCF-7), demonstrating a positive correlation between IL-8 expression and the metastatic capacity of mammary carcinoma cell lines (De Larco *et al.*, 2001, Lin *et al.*, 2004). In a tumor xenograft model, IL-8 expressing cells formed larger tumors than the control cells with enhanced microvessel density and

increased IL-8 expression was associated with the tumor growth and angiogenesis of breast cancer (Lin *et al.*, 2004, Zhou *et al.*, 2006).

In addition to metastatic potential of IL-8, the expression of TFF3 in mammary carcinoma is an predictive biomarker for metastasis (Ahmed *et al.*, 2012). TFF3 has also been identified as a promoter of metastatic dissemination of mammary carcinoma cells (Pandey *et al.*, 2014). The expression of TFF3 is positively associated with the metastatic phenotype in mammary carcinoma cells. Increased expression of TFF3 is associated with invasion of muscle, the nipple, neural sheath, and the lymphovasculture (Ahmed *et al.*, 2012). Increased TFF3 expression stimulated mammary carcinoma cells to metastasize away from the primary tumor and penetrated into the lymphovasculture followed by forming of micrometastatic breast cancer (Ahmed *et al.*, 2012).

I have observed that mammary carcinoma cells with forced expression of TFF3 expressed CXCR1 and CXCR2 mRNAs. Numerous of studies have demonstrated that the differential expression of IL-8 receptors between benign and malignant breast cancer tissues. A clinical study by Miller *et al.* (1998) reported that all breast cancer cells expressed IL-8 receptors, CXCR1 and CXCR2. In contrast, Freund *et al.* (2003) observed that CXCR1 expression is extremely low in mammary carcinoma cell lines, but most of the cells expressed CXCR2, without any correlation with ER status (Freund *et al.*, 2003). Notably, IL-8 receptors expressed in many human cancer cells with no apparent correlation with the grade of the tumor (Miller *et al.*, 1998, Muller *et al.*, 2001).

The tumor promoting effects of IL-8 in modulating the survival, angiogenesis, and metastasis of cancer cells were attenuated by humanized anti-IL-8 monoclonal antibodies (Fujisawa *et al.*, 2000, Li *et al.*, 2003a). Depletion of IL-8 in human melanoma cell lines by anti-sense RNA has revealed that IL-8 may function as a growth modulator (Schadendorf *et al.*, 1993). Administration of humanized monoclonal antibodies against IL-8 (e.g., ABX-IL-8) attenuated the growth of bladder cancer (Mian *et al.*, 2003) and decreased tumorigenic and metastatic potential of melanoma in xenograft models (Huang *et al.*, 2002). IL-8 gene

silencing by siRNA has been exploited to deplete IL-8 expression in ovarian tumor xenograft models, resulting in growth retardation and reduced microvessel density (Merritt *et al.*, 2008). Concordantly, I have demonstrated that depletion of IL-8 in mammary carcinoma cells by siRNA or inhibition of IL-8 with anti-IL-8 monoclonal antibody abrogated the ability of TFF3 to stimulate angiogenic behaviors of HUVEC. Additionally, inhibition of IL-8 in mammary carcinoma cells by anti-IL-8 monoclonal antibody attenuated the effect of TFF3 on the stimulation of HUVEC tubule formation *in vitro* mediated by IL-8. Both IL-8 siRNA and anti-IL-8 monoclonal antibody were able to inhibit the ability of TFF3 to stimulate angiogenic behaviors of HUVEC for promoting *de novo* angiogenesis in mammary carcinoma.

IL-8 receptors in the endothelial cells have been shown to be involved in tumor angiogenesis (Singh *et al.*, 2010). IL-8 binds to its cognate receptors either CXCR1 or CXCR2 and subsequently promotes endothelial cell proliferation and tumor angiogenesis. Administration of neutralizing antibodies against to CXCR1 and CXCR2 in endothelial cells abrogated tubule formation stimulated by IL-8, indicating that these two receptors are critical for activation of angiogenic responses of IL-8 (Salcedo *et al.*, 2000a, Li *et al.*, 2005). Other studies have also supported the importance of CXCR1 and CXCR2 in tumor angiogenesis (Varney *et al.*, 2006, Singh *et al.*, 2009). Of these two high affinity receptors, CXCR2 receptor in the endothelial cells is more prone to implicate in tumor angiogenesis stimulated by IL-8 (Addison *et al.*, 2000, Strieter *et al.*, 2004). I have observed that blocking of CXCR1 in the HUVEC by anti-CXCR1 monoclonal antibody was probably not able to inhibit the effect of TFF3 on the stimulation of HUVEC tubule formation *in vitro*. However, blocking of CXCR2 in the HUVEC by anti-CXCR2 monoclonal antibody abrogated the ability of TFF3 to stimulate HUVEC tubule formation *in vitro* mediated by IL-8 through CXCR2. It is known that CXCR2 has other chemokine ligands such as IL-1, IL-2 and IL-6 (Addison *et al.*, 2000). It is possible that anti-CXCR2 is disrupting IL-8-independent events. These observations were concordant with Heidemann *et al.* (2003) that IL-8 promoted angiogenesis in the human intestinal microvascular endothelial cells is dependent on CXCR2, a receptor targeted by

multiple angiogenic CXC chemokines. Other studies have also reported that the migration of endothelial cells can be suppressed by neutralizing antibody to CXCR2 (Schraufstatter *et al.*, 2001, Li *et al.*, 2005) and delayed vascularization in CXCR2 knockout mice (Devalaraja *et al.*, 2000). Therefore, I suggested that TFF3 stimulates angiogenic behaviors of HUVEC for promoting *de novo* angiogenesis in mammary carcinoma mediated by IL-8 through CXCR2 axis.

(ii) STAT3 partially mediated angiogenic behaviors of endothelial cells stimulated by TFF3

IL-8 promoter activity is regulated by the differential binding of the transcription factors namely NF-IL-6, NF- κ B, and AP-1 (Mukaida *et al.*, 1990, Roebuck, 1999) and several other nuclear factors such as hepatocyte nuclear factor-1 and glucocorticoid-responsive element (Mukaida *et al.*, 1989). The regulatory elements in the proximal region of IL-8 gene are important for activation of IL-8 promoter activity (Kashima *et al.*, 2009). The 5'-flanking region of the IL-8 contains DNA response elements for transcription factors NF-IL-6 (-94 to -81 bp), AP-1 (-126 to 120 bp) and NF- κ B (-80 to -70 bp) (Mukaida *et al.*, 1994). These three transcription factors binding sites are the major elements involved in the regulation of the IL-8 and their physical proximity may facilitate cooperative activation of these elements (Roebuck, 1999). Concordantly, I have demonstrated that TFF3 stimulated IL-8 promoter activity and subsequently increased IL-8 expression. Additionally, the transcription factors namely NF-IL-6, AP-1 and NF- κ B, present at the proximal region of IL-8 promoter, were involved in enhancing TFF3-stimulated IL-8 promoter activity. Apparently, multiple transcription factors are involved in the regulation of IL-8 stimulated by TFF3.

The production of IL-8 is modulated by activation of IL-8 promoter via cooperation of multiple transcription factors (Le *et al.*, 2000). It has been reported that increased IL-8 expression was predominantly stimulated by NF- κ B (Karashima *et al.*, 2003). Constitutive IL-8 expression required both NF- κ B and STAT3, over-expression of activated STAT3 resulted in a drastically increase of IL-8 protein expression (Scholz *et al.*, 2003). The

Src/STAT3 pathways may promote IL-8 production independent of NF- κ B (Trevino *et al.*, 2006). Gharavi *et al.* (2007) suggested that either STAT3 alone is adequate or a different co-activator such as NF- κ B is required to cooperate with STAT3 for stimulation of IL-8 expression in cancer cells (Gharavi *et al.*, 2007). STAT3 is an important regulatory element involved in the regulation of IL-8 and STAT3 presumably direct interaction with its consensus binding site at the IL-8 promoter region (Oka *et al.*, 2010). Concordantly, Seidel *et al.* (1995) has reported that a putative STAT3 binding site was predicted in the 5'-flanking region of IL-8 gene (Seidel *et al.*, 1995).

Herein, I have demonstrated that forced expression of TFF3 in mammary carcinoma cells increased tyrosine phosphorylation of STAT3 protein (Y705 pSTAT3). This observation was consistent with a recent study shown that TFF3 promoted STAT3 activity in mammary carcinoma cells through activation of c-Src protein (Pandey *et al.*, 2014). Depletion of STAT3 by siRNA partially abrogated the ability of TFF3 to stimulate IL-8 promoter activity and resulted in a small decreased of IL-8 expression. Additionally, depletion of STAT3 in mammary carcinoma cells by siRNA partially abrogated the ability of TFF3 to stimulate angiogenic behaviors of HUVEC mediated by STAT3. Furthermore, TFF3 was shown to promote a mesenchymal and invasive (EMT) phenotype to enhance the metastatic capability of mammary carcinoma cells through c-Src/STAT3 signaling pathway by activation of EMT markers (Pandey *et al.*, 2014). Thereby, forced expression of TFF3 down-regulated the expression of E-cadherin and concomitantly increased expression of vimentin to promote metastatic dissemination of mammary carcinoma cells (Pandey *et al.*, 2014).

A number of reports have shown that STAT3 plays a pivotal role in tumor angiogenesis by enhancing VEGF protein expression (Niu *et al.*, 2002, Osugi *et al.*, 2002, Schaefer *et al.*, 2002). STAT3 activity is regulated by post-translational modifications involving phosphorylation of specific conserved tyrosine residues (e.g., tyrosine 705) and active nuclear translocation followed by DNA binding and transcriptional activation of the target genes (Jove, 2000). The constitutively active STAT3 directly acts on VEGF-A gene to

stimulate VEGF-A promoter activity and subsequently up-regulates VEGF-A expression to stimulate neovascularization in the tumors (Niu *et al.*, 2002). Similarly, STAT3 may be able to directly act on the IL-8 promoter to regulate IL-8 expression. Several studies have suggested that IL-8 promoter may be containing a putative consensus binding site for STAT3, which is involved in the regulation of IL-8 (Seidel *et al.*, 1995, Oka *et al.*, 2010). Presumably, TFF3 secreted from mammary carcinoma cells stimulated tyrosine phosphorylation of STAT3, the activated STAT3 dimerizes, translocates into the nucleus, and directly binds to the IL-8 promoter for regulation of IL-8 gene transcription (Bromberg *et al.*, 1999, Garcia *et al.*, 2001, Niu *et al.*, 2002, Rivat *et al.*, 2005). Mechanistically, I suggested that forced expression of TFF3 in mammary carcinoma cells elevated IL-8 expression and increased the phosphorylated STAT3 activity. Subsequently, TFF3 stimulated angiogenic behaviors of endothelial cells for promoting *de novo* angiogenesis in mammary carcinoma through IL-8/CXCR2 axis. Hence, TFF3 is a promoter of angiogenesis, which may also co-coordinate with the growth promoting and metastatic actions of TFF3 in mammary carcinoma to enhance tumor progression.

CHAPTER 4

Exogenous Human Recombinant TFF3 and TFF3 Secreted from HUVEC Promoted Angiogenesis

4.1 Introduction

Angiogenesis is a complex and sequential process in which the existing blood vessel generates new vasculature. Following stimulation of endothelial cells by angiogenic factors, the endothelium is destabilized, producing a decrease in endothelial cell adhesion and a concomitant increase in vascular permeability (Petreaca *et al.*, 2007). The basal lamina of blood vessel is then degraded by matrix metalloproteinases to allow the endothelial cells to proliferate and migrate into surrounding connective tissues. The endothelial cells then sprout from adjacent vessel and fuse to produce a labyrinth of new blood vessels (Petreaca *et al.*, 2007). The nascent vessel recruits periendothelial and smooth muscle-like cells to stabilize the endothelium by promotion of the depositions of basal lamina and intercellular adhesion (Daniel and Abrahamson, 2000, Conway *et al.*, 2001). Angiogenesis is critical for different physiological and pathophysiological processes, including embryonic development, wound healing and chronic inflammation, and cancer progression (Folkman, 1995).

Under normal physiological conditions, angiogenesis is a tightly regulated process in which quiescent endothelial cells are induced to divide, leading to the spread of the vascular network, which supplies oxygen and nutrients to the growing tissues. Normal angiogenesis occurs during embryogenesis where it establishes the primary vasculature and generates adequate blood vessels for development of organs (Folkman, 1995). *De novo* angiogenesis is important in normal physiological repair mechanisms such as wound healing (Klagsbrun and D'Amore, 1991). The angiogenic switch in cancer is coordinated by the combinatorial balance between pro- and anti-angiogenic factors, produced either by cancer cells or by stromal cells in the surrounding interstitium (Baeriswyl and Christofori, 2009).

It is already known that angiogenic factors derived from a tumor are implicated in *de novo* angiogenesis, but there is evidence showed that angiogenic factors and the endothelial cells are pivotal origins of signals to non-vascular tissue cells during development of organs (Crivellato, 2011). Endothelial cells produce a number of secreted angiogenic proteins that enhance migration, survival and function of neighboring cells (e.g. mature endothelial cells), thereby promoting neovascularization. Furthermore, endothelial cells are crucial participants in tumor angiogenesis (Harvey *et al.*, 2002).

The expression of the TFF family of protein has been observed in tissues containing mucus-secreting cells as exemplified by the gastrointestinal tract, and colon, suggesting that their physiological functions may be related to that of mucin (Kraljevic Pavelic *et al.*, 2011). Importantly, these peptides are involved in the protection of the gastrointestinal tract against mucosal damage and in mucosal restitution (Taupin and Podolsky, 2003). In addition, TFF peptides are expressed in other organs including lymphoid tissue (Cook *et al.*, 1999), brain (Probst *et al.*, 1996, Jagla *et al.*, 2000), liver and gall bladder (Sasaki *et al.*, 2007). Thus, the functions of TFF peptides are cell-type specific. TFF peptides are secreted from diverse organs and exert different functional effects, yet their biological significance for most part is still elusive (Kjellev, 2009). *In vitro* experimental data have shown that exogenous recombinant human TFF3 (rhTFF3) stimulated migration of intestinal, respiratory and corneal epithelial cells in wound healing assays (Chinery and Playford, 1995, Playford *et al.*, 1995, Göke *et al.*, 2001, Oertel *et al.*, 2001, Graness *et al.*, 2002). Extracellular administration of rhTFF3 provides protection against ethanol-induced gastric mucosal damage and drug-induced intestinal mucosal injury (Kindon *et al.*, 1995, Playford *et al.*, 1996, McKenzie *et al.*, 2000, Babyatsky *et al.*, 2009). Furthermore, functional studies of TFF3 on epithelial mucosal damage have shown that rhTFF3 potently stimulated the migration of intestinal epithelial cells, promoted wound healing, and altered E-cadherin expression to enhance the migration of epithelial cells (Dignass *et al.*, 1994, Playford *et al.*, 1995).

A study by Rodrigues *et al.* (2003b) demonstrated that exogenous rhTFF3 promoted capillary vessel formation in a CAM assay, suggesting that TFF3 may function as pro-angiogenic factor. Moreover, the angiogenic activity of TFF1 in HUVEC tubule formation *in vitro* was comparable to that stimulated by VEGF-A. TFF1 promoted angiogenesis *in vitro* which mediated by both cyclooxygenase-2 (COX-2) and epidermal growth factor receptor (EGF-R) (Rodrigues *et al.*, 2003b). Given that TFF3 is analogous to TFF1, TFF3 may possess similar pro-angiogenic characteristic as TFF1, suggesting that TFF3 may also be involved in angiogenesis *in vivo*, although further studies are required to determine whether TFF3 can directly act on endothelial cells to stimulate its angiogenic behaviors.

HUVEC are preferable to use as a cell-based model for study of angiogenesis *in vitro* as they retain the traits or functional characteristics of normal human endothelial cells (Ades *et al.*, 1992, Bouis *et al.*, 2001). HUVEC possesses the ability to form tubule in the basement membrane extract Matrigel resembles to the ECM, thus mimicking angiogenesis *in vitro* (Donovan *et al.*, 2001, Auerbach *et al.*, 2003, Bagley *et al.*, 2003). HUVEC tubule formation *in vitro* is a simple, feasible and reproducible assay and commonly used to determine the angiogenic potential an angiogenic factor (Okamura *et al.*, 1992, Ito *et al.*, 1995). HUVEC are grown in the Matrigel in the presence of a tested angiogenic protein and subsequently lead to either promotion or inhibition of tubule formation, indicating that the angiogenic protein can directly stimulate or inhibit angiogenic behaviors of HUVEC (Aranda and Owen, 2009). The angiogenic potential of an angiogenic protein can be quantified by measuring tubule length and/or tubule number (Jones *et al.*, 1998).

In this study, the immortalized human umbilical vein endothelial cells (HUVEC) were utilized as an *in vitro* endothelial model. HUVEC with forced expression of TFF3 were generated by transient transfection with a pIRESneo3 (Invitrogen, Carlsbad, CA) expression vector containing human TFF3 cDNA (NM_003226) (designated as HUVEC-TFF3), or the pIRESneo3 empty vector (designated as HUVEC-Vec). HUVEC with depletion of TFF3 were generated by transient transfection of HUVEC with a pSilencer 2.1-U6 hygro (Ambion,

Austin, TX) expression vector containing TFF3 siRNA (designated as HUVEC-siTFF3), or with control siRNA encoding a siRNA that has no significant sequence similarity to human gene sequences (designated as HUVEC-siVec).

I therefore postulate that exogenous rhTFF3 directly acts on HUVEC to promote angiogenic behavior of HUVEC and TFF3 secreted from HUVEC may also exert similar functional effects as exogenous rhTFF3 in promoting of angiogenesis.

4.2 Results

4.2.1 Exogenous rhTFF3 increased HUVEC monolayer proliferation

Recombinant human TFF3 (rhTFF3) was expressed from pGEX-4T1-TFF3 plasmid in *E coli* and purified using glutathione-S-transferase tag affinity chromatography under non-reducing condition as previously described (Amiry *et al.*, 2009). The specificity and purity of this protein has been determined by Western blot analysis, whereby a single band was detected as a monomer at 7 kDa or dimer at 14 kDa under reducing and non-reducing conditions, respectively (Amiry *et al.*, 2009).

Different concentrations of rhTFF3 (0.1, 1.0, 2.5, 5.0, and 10.0 ng/mL) were used to examine the effect of exogenous rhTFF3 stimulation on HUVEC monolayer proliferation. The effect of exogenous rhTFF3 on HUVEC monolayer proliferation (total cell number) after 48 hours with different concentration of rhTFF3 in 0.2% FBS (serum deprived) and 10% FBS (serum replete) conditions were determined. Exogenous rhTFF3 stimulation significantly increased HUVEC monolayer proliferation from 35% at 2.5 ng/mL rhTFF3 to 100% at 10.0 ng/mL rhTFF3 in 10% FBS conditions when compared with HUVEC treated with BSA control protein (Figure 47A). Lower concentration of exogenous rhTFF3 may not able to stimulate HUVEC monolayer proliferation in serum deprived conditions (0.2% FBS), but slightly increased HUVEC monolayer proliferation by 18% at a higher concentration of rhTFF3 (10 ng/mL) (Figure 47B), indicating that exogenous rhTFF3 promoted HUVEC monolayer proliferation in a concentration-dependent manner.

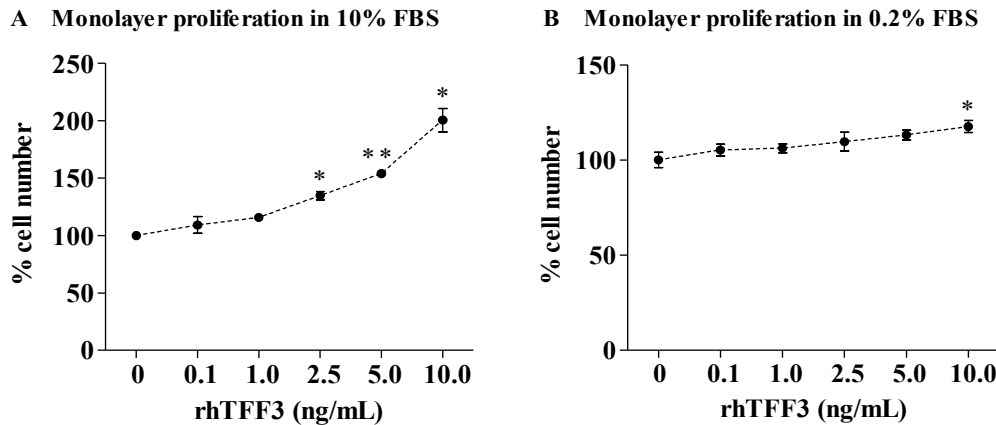


Figure 47: Exogenous rhTFF3 stimulation increased monolayer proliferation of HUVEC. A, HUVEC monolayer proliferation at different concentrations of rhTFF3 (0.1, 1.0, 2.5, 5.0, 5, 10 ng/mL of rhTFF3) in 10% FBS condition. B, HUVEC monolayer proliferation at different concentrations of rhTFF3 (0.1, 1.0, 2.5, 5.0, 5, 10 ng/mL of rhTFF3) in 0.2% FBS condition. Different concentrations of rhTFF3 in 0.2% FBS or 10% FBS EBM media was added to the HUVEC and incubated at 37°C for 48 hours. BSA was used as control. HUVEC treated with 10 ng/mL BSA was used as baseline. *, $P < 0.05$; **, $P < 0.01$ as compared with BSA control.

4.2.2 Exogenous rhTFF3 stimulation increased HUVEC migration, invasion, and tubule formation *in vitro*

To determine whether the exogenous rhTFF3 stimulation acted as a chemoattractant or stimulant, a transwell migration assay was performed to examine the effect of exogenous rhTFF3 stimulation on HUVEC migration. The untreated HUVEC plated in the membrane of the transwell insert incubated with 5.0 ng/mL rhTFF3 in the bottom well of the companion plate increased HUVEC migration as compared to the HUVEC incubated with BSA control and therefore rhTFF3 acted as a chemoattractant (Figure 48A). Alternatively, HUVEC treated with 5 ng/mL rhTFF3 plated in the membrane of transwell insert and incubated with 10% FBS EBM medium in the bottom well of the companion plate also increased HUVEC migration as compared to the HUVEC incubated with BSA control and therefore rhTFF3 acted as stimulant of migration (Figure 48A). Exogenous rhTFF3 acted as both a chemoattractant and stimulant to induce migratory behavior of HUVEC and to promote HUVEC migration. Notably, the chemoattractant effect of rhTFF3 on the HUVEC migration is more significant than the stimulant effect of rhTFF3. Subsequently, the effect of different

concentrations of rhTFF3 (0.1, 1.0, 2.5, 5.0, 10.0 ng/mL of rhTFF3) on HUVEC migration and invasion was determined. HUVEC were plated in the membrane of the transwell insert and incubated with different concentrations of rhTFF3 or BSA control in the bottom well of the companion plate. As compared to HUVEC incubated with BSA control, exogenous rhTFF3 significantly increased HUVEC migration from 45% to 104% at varying concentrations of rhTFF3 (2.5, 5.0, 10.0 ng/mL of rhTFF3), with the maximal HUVEC migration observed at 5.0 ng/mL of rhTFF3 (Figure 48B). Additionally, exogenous rhTFF3 stimulation significantly increased HUVEC invasion from 47% to 52% at varying concentrations of rhTFF3 (2.5, 5.0, 10.0 ng/mL of rhTFF3), with maximal HUVEC invasion at 5.0 ng/mL of rhTFF3 as compared with HUVEC incubated with BSA control (Figure 48C). These observations indicated that exogenous rhTFF3 promoted HUVEC migration and invasion in a concentration-dependent manner, with maximal stimulation at 5.0 ng/mL rhTFF3.

To determine the effect of exogenous rhTFF3 stimulation on HUVEC tubule formation *in vitro*, HUVEC plated in the Matrigel were treated with different concentrations of rhTFF3 (0.1, 1.0, 2.5, 5.0, 10.0 ng/mL of rhTFF3). Exogenous rhTFF3 stimulation significantly increased tubule length formed by HUVEC from 48% to 69% at varying concentration of rhTFF3 (1.0, 2.5, 5.0 ng/mL of rhTFF3), with maximal HUVEC tubule formation *in vitro* at 5.0 ng/mL (Figure 48D-E). Higher concentration of rhTFF3 (10.0 ng/mL) exhibited a slight increase of tubule length formed by HUVEC (22%) when compared with HUVEC treated with control BSA. These observations suggested that exogenous rhTFF3 stimulation significantly increased HUVEC tubule formation *in vitro* with maximal stimulation at 5.0 ng/mL of rhTFF3 and exhibited lesser stimulatory effect on HUVEC tubule formation *in vitro* at a higher concentration of exogenous rhTFF3.

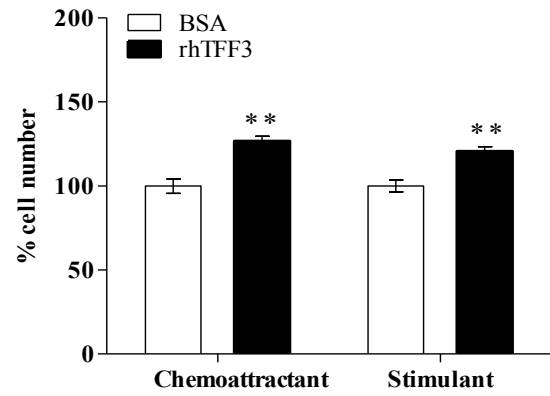
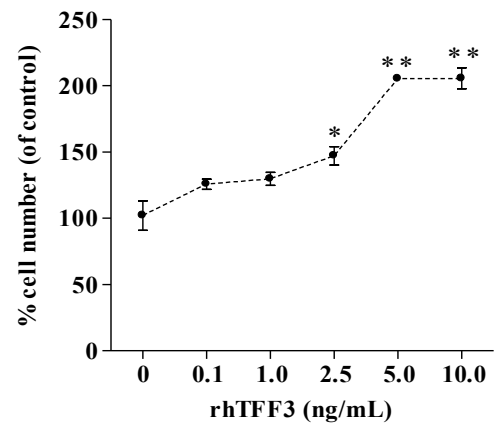
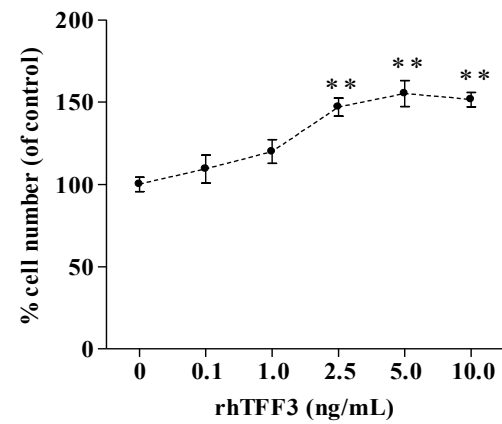
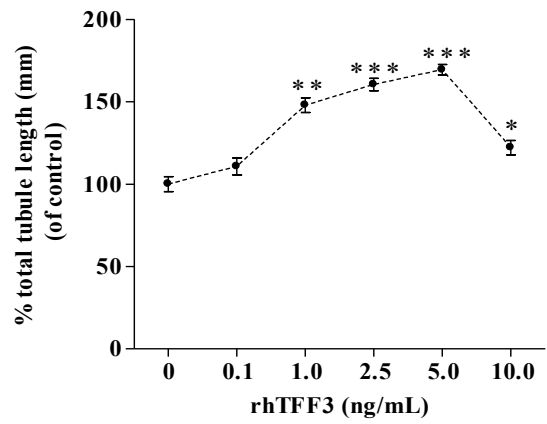
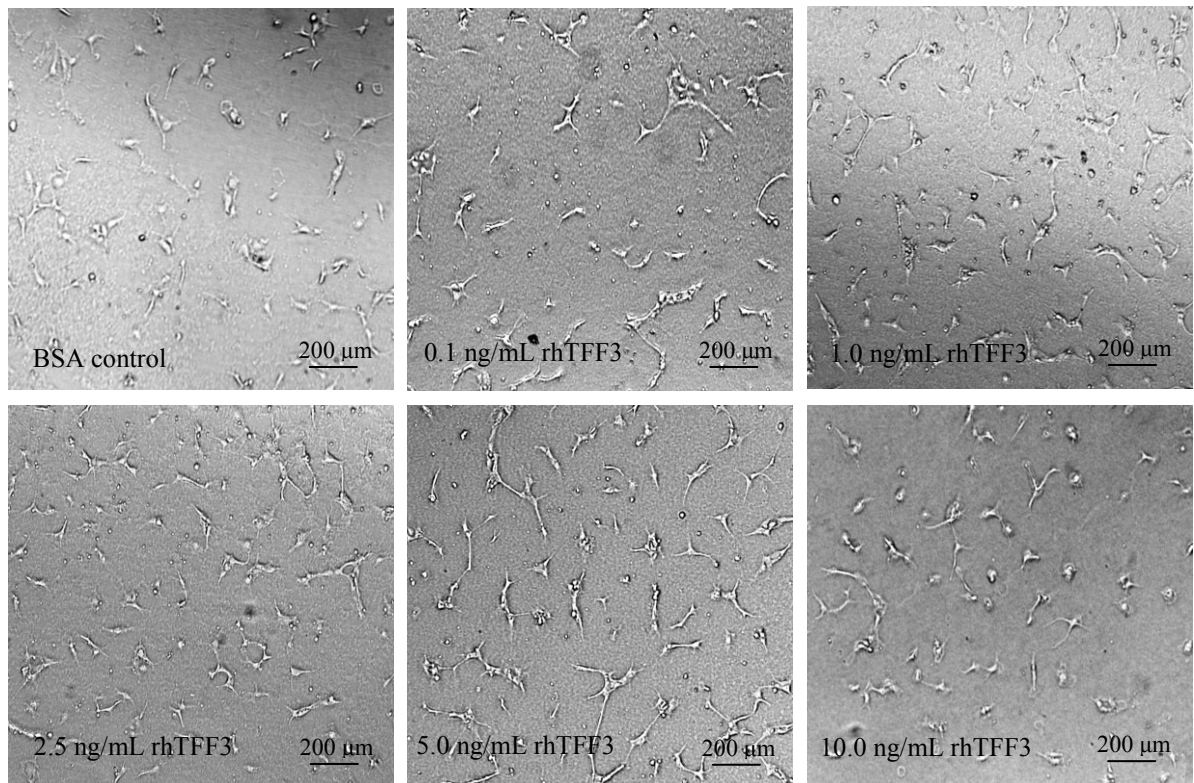
A Migration**B Migration****C Invasion****D Tubule length****E Tubule formation**

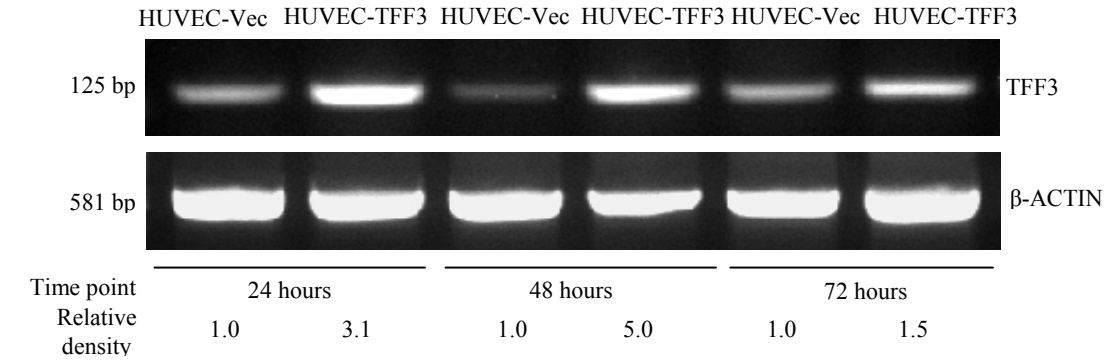
Figure 48: Exogenous rhTFF3 stimulation increased HUVEC migration, invasion, and tubule formation *in vitro*. A, Exogenous rhTFF3 acted as chemoattractant and stimulant on HUVEC migration. For rhTFF3 to act as a chemoattractant, HUVEC were plated on the membrane of a transwell insert and incubated with either exogenous rhTFF3 (5 ng/mL) or BSA used as a control (5 ng/mL) in the bottom well of companion plate for 24 hour. For rhTFF3 to act as a stimulant, 5 ng/mL rhTFF3 or BSA control was added to the HUVEC were plated on the membrane of a transwell insert and incubated with 10% FBS EBM medium in bottom well of companion plate of for 24 hour. B, Migration of HUVEC after 24 hour incubation with different concentration of exogenous rhTFF3 (0.1, 1.0, 2.5, 5, 10 ng/mL of rhTFF3) or BSA control (10 ng/mL). C, Invasion of HUVEC after 24 hours incubation with different concentration of exogenous rhTFF3 (0.1, 1.0, 2.5, 5, 10 ng/mL of rhTFF3) or BSA control (10 ng/mL). D, Exogenous rhTFF3 stimulation in the HUVEC tubule formation *in vitro*. HUVEC plated in the Matrigel were treated with different concentration of exogenous rhTFF3 (0.1, 1.0, 2.5, 5, 10 ng/mL of rhTFF3) or BSA control (10 ng/mL). Total tubule length was assessed after 12 hour using ImageJ analysis software. E, representative light microscopy images of HUVEC tubule formation *in vitro* in which HUVEC treated with different concentrations of rhTFF3 or BSA control. BSA was used as control. HUVEC treated with BSA control was used as baseline. The light microscopy images were taken at $\times 40$. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$ as compared with BSA control; scale bar, 200 μm .

4.2.3 Forced expression of TFF3 in HUVEC increased TFF3 expression

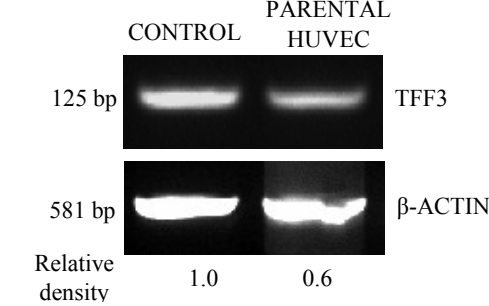
I have demonstrated that exogenous rhTFF3 stimulation directly acted on HUVEC to promote angiogenic behaviors *in vitro*. I then determined whether TFF3 secreted from HUVEC exerted similar functional activity as exogenous rhTFF3 to promote the angiogenic behaviors of endothelial cells. HUVEC were transiently transfected with an expression vector containing TFF3 cDNA (designated as HUVEC-TFF3) or pIRESneo3 empty vector (designated as HUVEC-Vec). Forced expression of TFF3 in HUVEC increased TFF3 mRNA as compared with control HUVEC-Vec after 24 hours transfection and the expression of TFF3 mRNA in HUVEC, though slightly decreased as compared to the 24 hour of post-transfection, was maintained until 72 hours of post-transfection (Figure 49A). Nevertheless, HUVEC with forced expression of TFF3 exhibited higher TFF3 mRNA than the control HUVEC-Vec from 24 hours to 72 hours post-transfection. Parental HUVEC endogenously expressed undetectable or very low level of TFF3 mRNA (Figure 49B) and protein (Figure 49C) as compared to the control (MCF-7 cells). HUVEC endogenously secreted TFF3 protein to the medium and was detected by rabbit anti-TFF3 polyclonal antibody in Western blot analysis (Figure 49D). Furthermore, forced expression of TFF3 in HUVEC increased TFF3

mRNA (Figure 49E) as compared with control HUVEC-Vec. Concordantly, forced expression of TFF3 in HUVEC also increased TFF3 protein in cell lysate and secreted to the medium (Figure 49F).

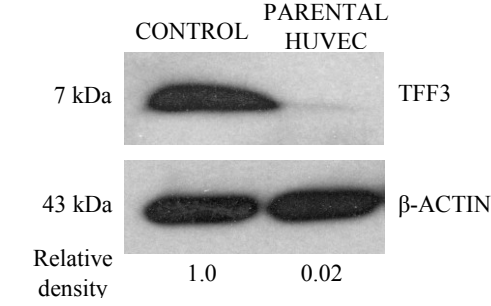
A RT-PCR



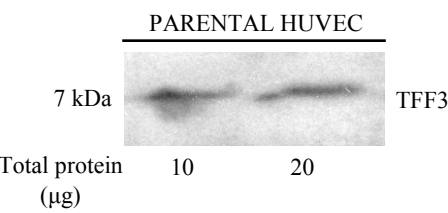
B RT-PCR



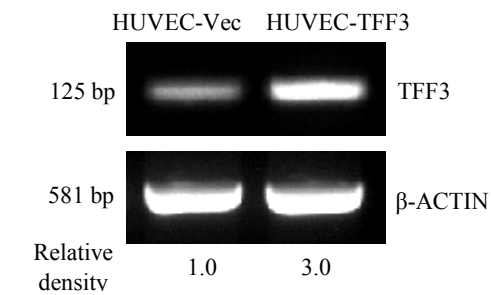
C Western blot



D Western blot



E RT-PCR



F Western blot

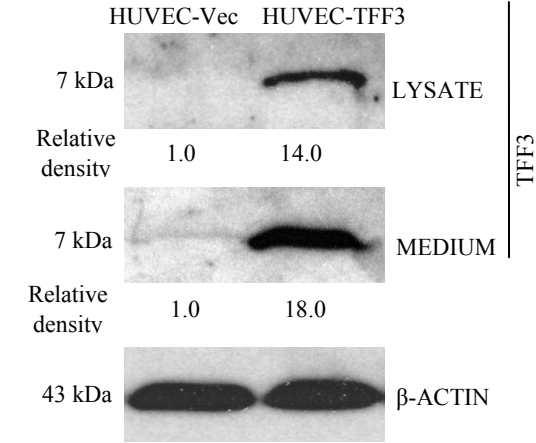


Figure 49: Forced expression of TFF3 in HUVEC increased TFF3 expression. A, Semi-quantitative RT-PCR analysis of TFF3 mRNA in HUVEC with forced expression of TFF3 after 24, 48, and 72 hours transfection. HUVEC with empty vector was used as control. B, Semi-quantitative RT-PCR analysis of TFF3 mRNA in parental HUVEC and control (MCF-7 cells). C, Western blot analysis of TFF3 protein in the cell lysate of HUVEC and control (MCF-7 cells). D, Western blot analysis of TFF3 protein in the medium of HUVEC which contained 10, 20 µg of total protein. E, semi-quantitative RT-PCR analysis of TFF3 mRNA in HUVEC with forced expression of TFF3. F, Western blot analysis of TFF3 protein in the cell lysate and conditioned medium of HUVEC with forced expression of TFF3. β -ACTIN was used as a loading control in both semi-quantitative RT-PCR and Western blot analysis.

4.2.4 Forced expression of TFF3 in HUVEC increased monolayer cell proliferation, cell cycle progression, survival

The effect of TFF3 secreted from HUVEC with forced expression of TFF3 on monolayer cell proliferation in both 10% FBS conditions (serum replete) for 72 hours and 0.2% FBS conditions (serum deprived) for 48 hours were determined. TFF3 secreted from HUVEC significantly increased monolayer cell proliferation in both 10% FBS and 0.2 % FBS conditions when compared with the control HUVEC-Vec (Figure 50A-B). When compared with control HUVEC-Vec, TFF3 secreted from HUVEC significantly increased monolayer cell proliferation by 29% in 10% FBS condition after 72 hours (Figure 50A) and by 30% in serum deprived conditions (0.2% FBS) after 48 hours (Figure 50B). These data indicated that TFF3 secreted from HUVEC promoted HUVEC monolayer cell proliferation in both 10% FBS and 0.2% FBS conditions. Furthermore, TFF3 secreted from HUVEC increased cell cycle progression, as indicated by BrdU incorporation, in both serum-free conditions and 10% FBS conditions by 30% and 43%, respectively, when compared with control HUVEC-Vec (Figure 50C). TFF3 secreted from HUVEC also decreased apoptotic cell death, as indicated by fluorescent microscopic nuclear staining, in both serum-free and 10% FBS conditions by 37% and 39%, respectively when compared with control HUVEC-Vec (Figure 50D). These data suggested that TFF3 secreted from HUVEC promoted cell proliferation and survival.

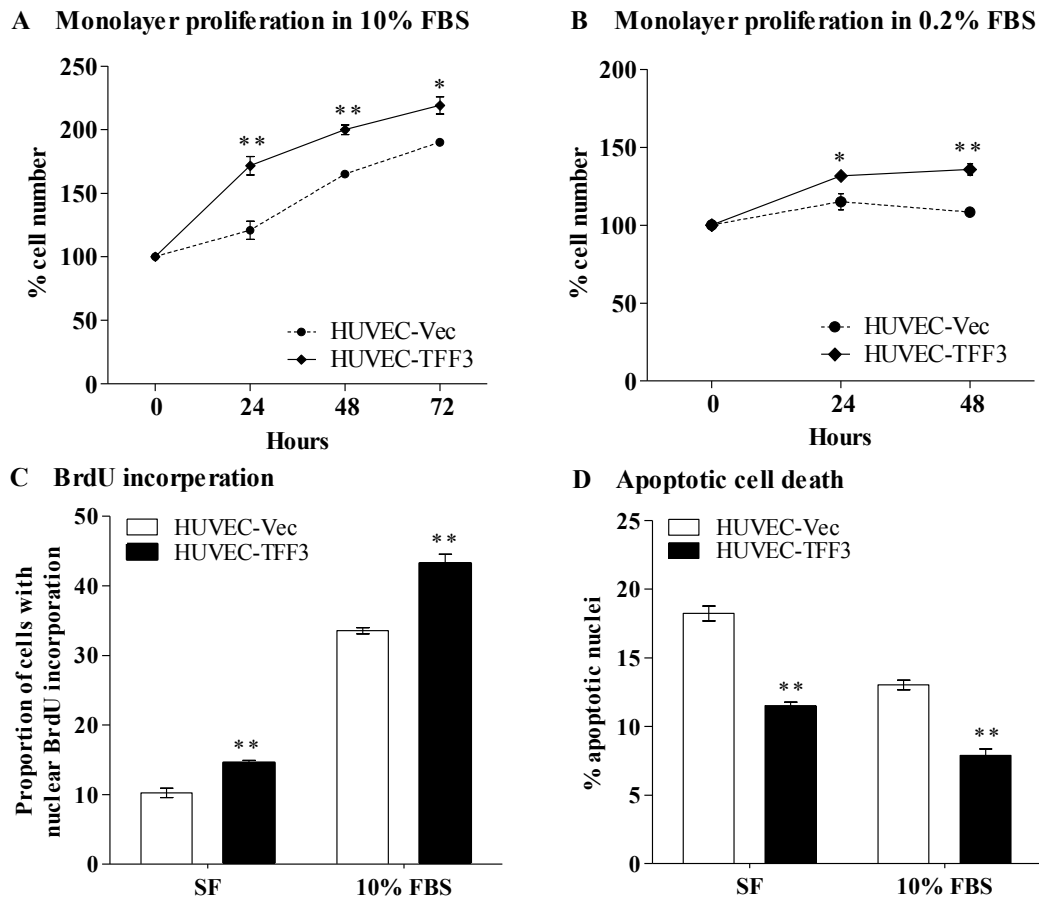


Figure 50: Forced expression of TFF3 in HUVEC increased monolayer cell proliferation, cell cycle progression, and survival. A, HUVEC monolayer cell proliferation after co-culture with HUVEC with forced expression of TFF3 in 10% FBS conditions. HUVEC with empty vector was used as control. B, HUVEC monolayer cell proliferation after co-culture with HUVEC with forced expression of TFF3 in 0.2% FBS condition. C, HUVEC cell cycle progression after 24 hours co-culture with HUVEC with forced expression of TFF3 in serum-free (SF) and 10% FBS conditions. D, HUVEC apoptotic cell death after 24 hours co-culture with HUVEC with forced expression of TFF3 in serum-free (SF) and 10% FBS conditions. *, $P < 0.05$; **, $P < 0.01$.

4.2.5 Forced expression of TFF3 in HUVEC increased migration, invasion, and tubule formation *in vitro*

To determine the effect of TFF3 secreted from HUVEC on the migratory and invasive behavior of endothelial cells, transwell migration and invasion assays were conducted. Forced expression of TFF3 in HUVEC consistently increased migration by 21% (Figure 51A) and invasion by 11% (Figure 51B) when compared with control HUVEC-Vec, suggesting that TFF3 secreted from HUVEC slightly promoted cell migration and invasion.

To determine whether TFF3 secreted from HUVEC stimulates angiogenesis *in vitro*, a tubule formation assay was conducted whereby HUVEC with forced expression of TFF3 were seeded in the Matrigel. TFF3 secreted from HUVEC significantly increased tubule length by 125% (Figure 51C) and tubule number by 56% (Figure 51D) when compared with control HUVEC-Vec. TFF3 secreted from HUVEC increased tubules formed by endothelial cells when compared with control HUVEC-Vec (Figure 51E), suggesting that TFF3 secreted from HUVEC promoted tubule formation *in vitro*.

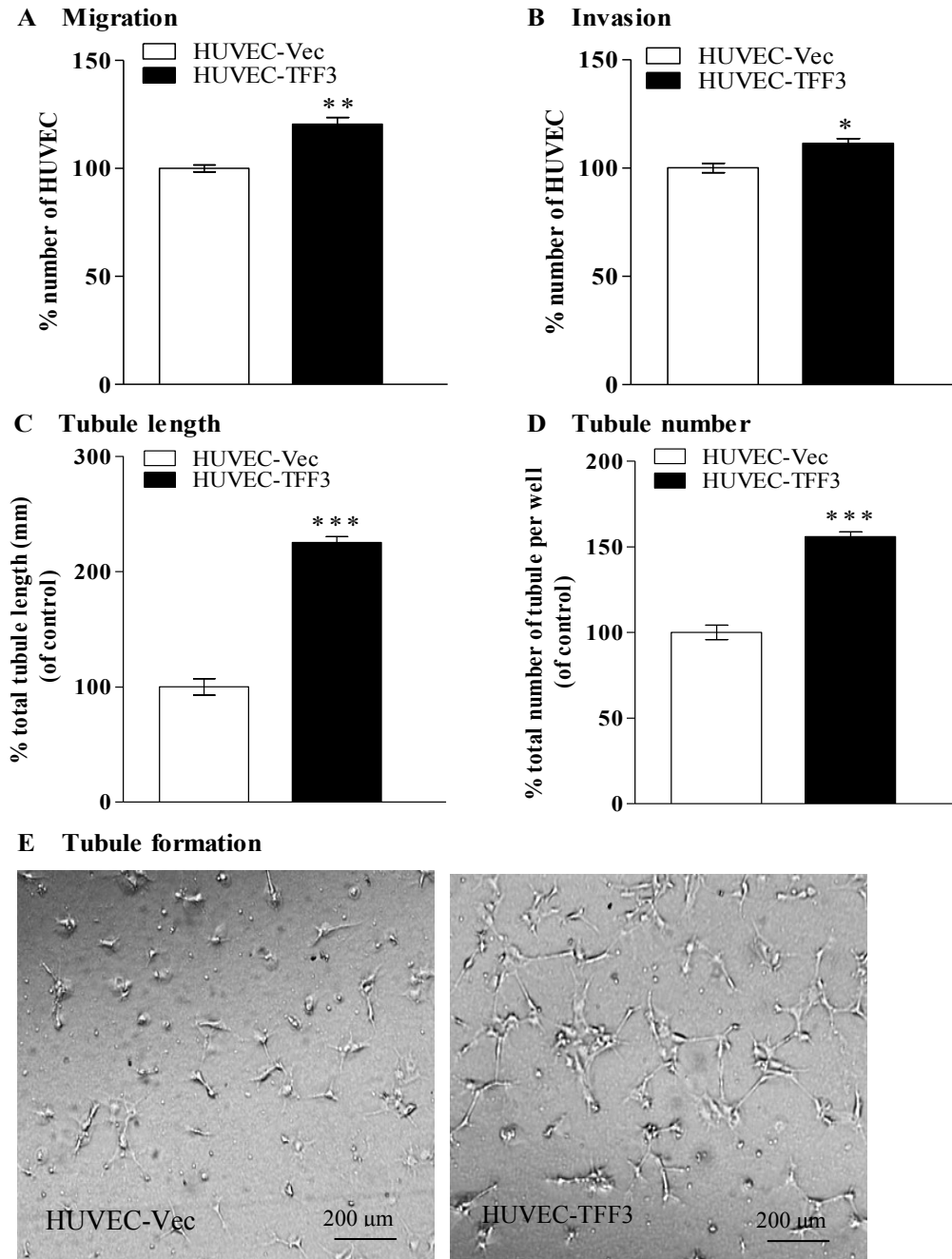


Figure 51: Forced expression of TFF3 in HUVEC increased cell migration, invasion, and tubule formation *in vitro*. A, HUVEC migration after 24 hours co-culture with HUVEC with forced expression of TFF3 in serum-free conditions. HUVEC with empty vector was used as control. B, HUVEC invasion after 24 hours co-culture with HUVEC with forced expression of TFF3 in serum-free conditions. C and D, tubule formation *in vitro* after 12 hours co-culture HUVEC with forced expression of TFF3 in the Matrigel. Total tubule length (C) and tubule number (D) were assessed using ImageJ analysis software. E, representative light microscopy images of tubule formation *in vitro* after 12 hours co-culture with HUVEC with forced expression of TFF3 in the Matrigel. The light microscopy images were taken at $\times 40$ magnification. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; scale bar, 200 μm .

4.2.6 Depletion of TFF3 in HUVEC by siRNA decreased TFF3 expression

To determine the effect of depletion of TFF3 on the angiogenic behaviors of endothelial cells, the endogenous expression of TFF3 in HUVEC was depleted by siRNA to TFF3. HUVEC were transiently transfected with an expression vector containing TFF3 siRNA (designated as HUVEC-siTFF3) or pSilencer 2.1-U6 hygro empty vector (designated as HUVEC-siVec). Depletion of TFF3 in HUVEC decreased TFF3 mRNA and protein when compared with control HUVEC-siVec (Figure 52A-B).

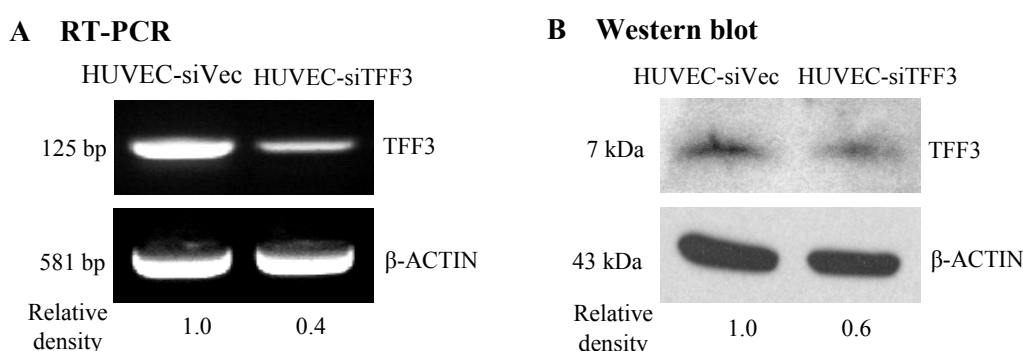


Figure 52: Depletion of TFF3 in HUVEC by siRNA decreased TFF3 expression. A, RT-PCR analysis of TFF3 mRNA in HUVEC with depletion of TFF3. HUVEC with control siRNA was used as control. B, Western blot analysis of TFF3 protein in HUVEC with depletion of TFF3. β-ACTIN was used as a loading control in both semi-quantitative RT-PCR and Western blot analysis.

4.2.7 Depletion of TFF3 in HUVEC decreased monolayer cell proliferation, cell cycle progression, and survival

The effect of TFF3 secreted from HUVEC with depletion of TFF3 by siRNA on monolayer cell proliferation in both 10% FBS conditions for 72 hours and 0.2% FBS conditions for 48 hours were determined. Depletion of TFF3 in HUVEC significantly decreased monolayer cell proliferation in both 10% FBS and 0.2% FBS conditions when compared with the control HUVEC-Vec (Figure 53A-B). When compared with the control HUVEC-siVec, depletion of TFF3 in HUVEC significantly decreased monolayer cell proliferation by 65% in 10% FBS condition (Figure 53A) and by 20% in serum deprived conditions after 48 hours (Figure 53B). Furthermore, depletion of HUVEC decreased cell

cycle progression in both serum-free conditions and 10% FBS conditions by 38% and 30%, respectively when compared with control HUVEC-Vec (Figure 53C). Depletion of TFF3 in HUVEC also increased apoptotic cell death in both serum-free conditions and 10% FBS conditions by 32% and 37%, respectively when compared with control HUVEC-Vec (Figure 53D). Depletion of TFF3 by siRNA in HUVEC decreased cell proliferation and survival.

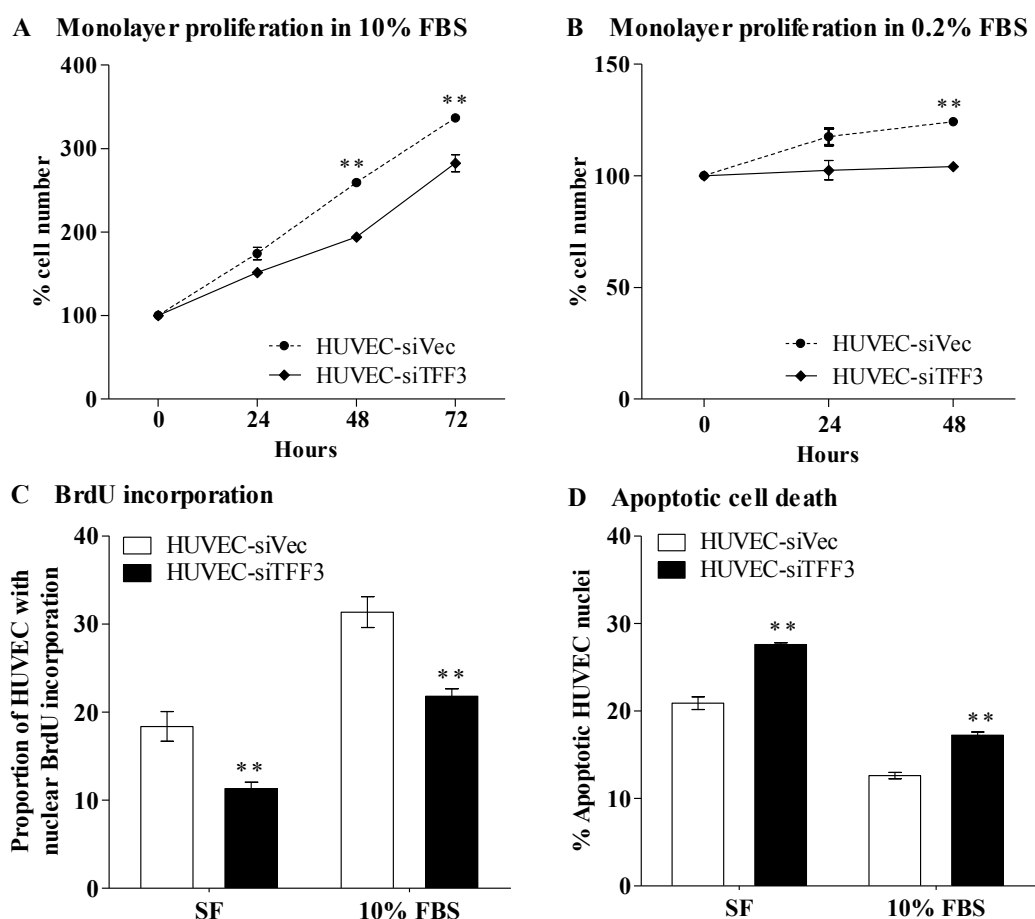


Figure 53: Depletion of TFF3 in HUVEC decreased monolayer cell proliferation, cell cycle progression, and survival. A, HUVEC monolayer cell proliferation after co-culture with HUVEC with depletion of TFF3 in 10% FBS conditions. HUVEC with control siRNA was used as control. B, HUVEC monolayer cell proliferation after co-culture with HUVEC with depletion of TFF3 in 0.2% FBS conditions. C, HUVEC cell cycle progression after co-culture with HUVEC with depletion of TFF3 in both serum-free (SF) and 10% FBS conditions. D, HUVEC apoptotic cell death after 24 hours co-culture with HUVEC with depletion of TFF3 in serum-free (SF) and 10% FBS conditions. *, $P < 0.05$; **, $P < 0.01$.

4.2.8 Depletion of TFF3 in HUVEC decreased migration, invasion, and tubule formation *in vitro*

The effect of depletion of TFF3 by siRNA on the angiogenic behaviors of HUVEC was determined. Depletion of TFF3 in HUVEC significantly decreased HUVEC migration by 37% (Figure 54A) and invasion by 28% (Figure 54B) when compared with control HUVEC-siVec. Furthermore, depletion of TFF3 by siRNA in HUVEC significantly decreased tubule length by 37% and tubule number by 38% when compared with control HUVEC-siVec (Figure 54C-D). Depletion of TFF3 in HUVEC decreased tubules formed by endothelial cells when compared with the control HUVEC-siVec (Figure 54E). Therefore, depletion of TFF3 by siRNA in HUVEC decreased angiogenic behaviors of endothelial cells.

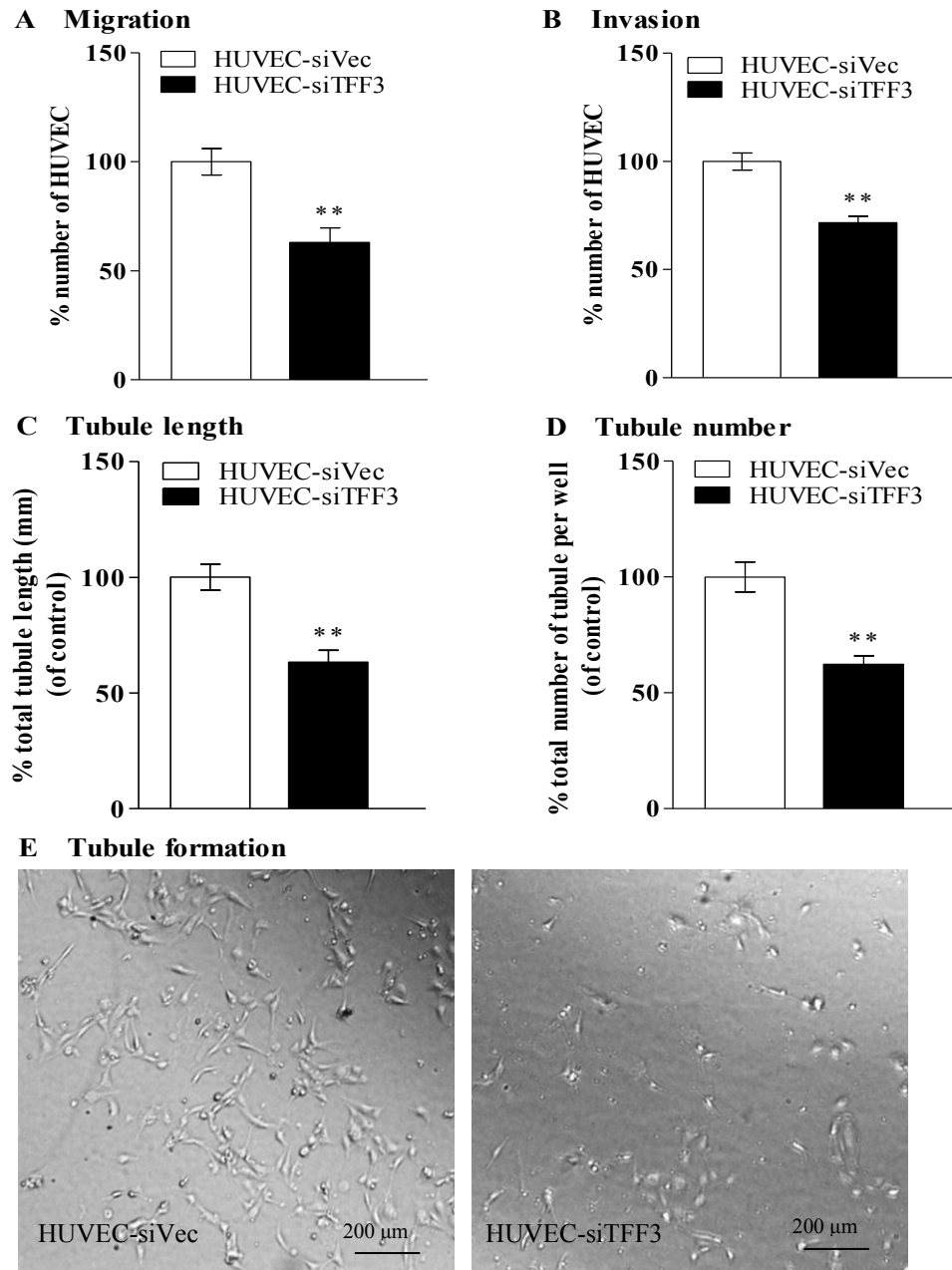


Figure 54: Depletion of TFF3 in HUVEC decreased migration, invasion, and tubule formation *in vitro*. A, cell migration after 24 hours co-culture with HUVEC with depletion of TFF3 in serum-free conditions. HUVEC with control siRNA was used as control B, cell invasion after 24 hours co-culture with HUVEC with depletion of TFF3 in serum-free conditions. C and D, tubule formation *in vitro* on Matrigel after 12 hours co-culture with HUVEC with depletion of TFF3 in serum-free conditions. Total tubule length (C) and tubule number (D) were assessed after 12 hours incubation using ImageJ analysis software. E, representative light microscopy images of tubule formation *in vitro* in the Matrigel after 12 hours co-culture with HUVEC with depletion of TFF3. The light microscopy images were taken at $\times 40$ magnification. **, $P < 0.01$; scale bar, 200 μ m.

4.2.9 Forced expression of TFF3 in HUVEC increased IL-8 promoter activity

To determine if TFF3 secreted from HUVEC regulated IL-8 promoter activity, HUVEC with forced expression of TFF3 were transiently transfected with an full length IL-8 promoter reporter vector (-4800 to +104 bp) and a pRL-CMV control reporter. Forced expression of TFF3 in HUVEC significantly increased IL-8 promoter activity (1.5-fold increase) as compared to the control HUVEC-Vec, indicating that TFF3 secreted from HUVEC stimulated IL-8 promoter activity, albeit slightly (Figure 55A). Additionally, HUVEC with forced expression of TFF3 transiently transfected with a shorter promoter, pGL-IL8-152 reporter vector (-152 to + 44 bp), significantly increased IL-8 promoter activity (2.0-fold increase) when compared with the control HUVEC-Vec (Figure 55B).

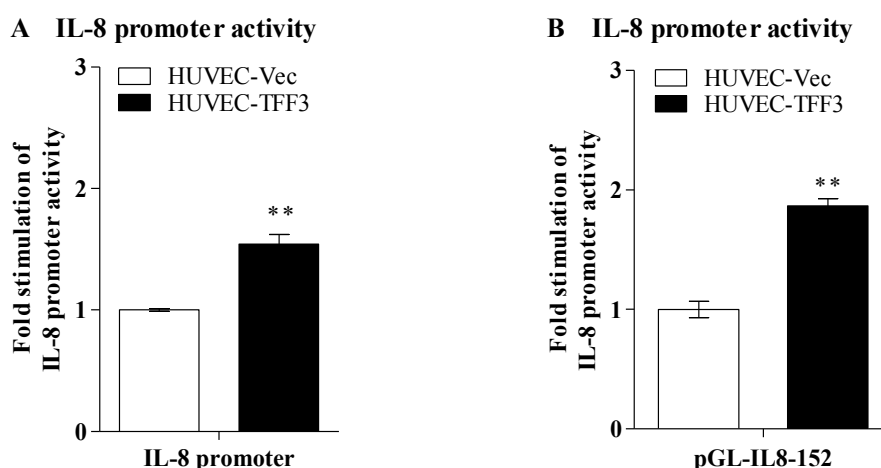


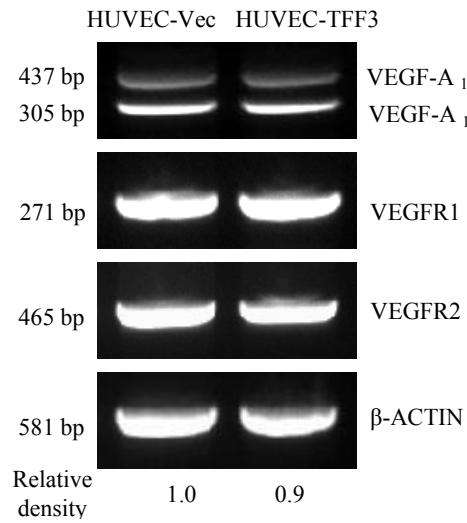
Figure 55: Forced expression of TFF3 in HUVEC increased IL-8 promoter activity. A, IL-8 promoter activity in HUVEC with forced expression of TFF3 transiently transfected with IL-8 promoter (full length, -4800 to + 104 bp). HUVEC with empty vector was used as control. B, IL-8 promoter activity in HUVEC with forced expression of TFF3 transiently transfected with pGL-IL8-152 reporter (-152 to +44 bp). Fragment containing 5' flanking regions of the IL-8 gene were subcloned upstream of a luciferase reporter gene in the pGL3-basic vector. pGL-IL8-152 reporter vector encompassing nucleotides -152 to +44 of the IL-8 promoter, which contain the transcriptional factors, AP-1, NF-IL6 and NF- κ B response site. The TATA box, and the NF-IL6, NF- κ B and AP-1 binding sites are located at -13, -70, -80 and -120, respectively. HUVEC with forced expression of TFF3 were transiently transfected with a reporter and a pRL-CMV control reporter. IL-8 promoter activity measured by firefly luciferase activity that normalized by *Renilla* luciferase activity. **, $P < 0.01$.

4.2.10 Forced expression of TFF3 in HUVEC increased IL-8 expression

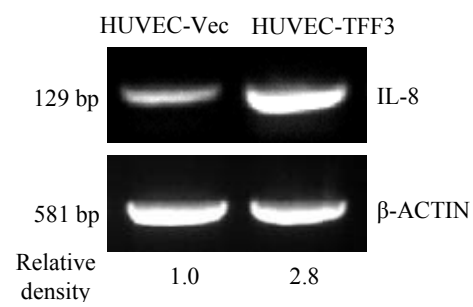
Forced expression of TFF3 in HUVEC stimulated angiogenic behaviors of HUVEC to promote angiogenesis *in vitro*. Presumably, TFF3 modulated the expression of one or more specific angiogenic factors that can mediate the angiogenic action of TFF3, in addition to the direct action of TFF3 on the HUVEC as previously demonstrated by exogenous rhTFF3 stimulation. Forced expression of TFF3 in HUVEC exhibited relatively similar expression levels of VEGF-A (VEGF-A₁₂₁ and VEGF-A₁₆₅ mRNAs) and its tyrosine kinase receptors (VEGFR1 and VEGFR2 mRNAs) when compared with the control HUVEC-Vec. Forced expression of TFF3 in HUVEC regulated neither the expression of VEGF-A₁₂₁ and VEGF-A₁₆₅ nor its tyrosine kinase receptors VEGFR1 and VEGFR2 (Figure 56A). The mRNA expressions of VEGF-A and VEGFR1/2 were observed in HUVEC. Nevertheless, forced expression of TFF3 in HUVEC increased IL-8 mRNA (Figure 56B) and protein (Figure 56C) when compared with the control HUVEC-Vec. Forced expression of TFF3 in HUVEC slightly increased IL-8 protein secreted to medium as compared with the control HUVEC-Vec (Figure 56D).

The angiogenic function of IL-8 is activated through the binding of IL-8 to its cognate receptors, termed as CXCR1 and CXCR2, which belong to the G protein-coupled receptor family (Holmes *et al.*, 1991). HUVEC with forced expression of TFF3 expressed both CXCR1 and CXCR2 mRNAs (Figure 56E). Forced expression of TFF3 in HUVEC slightly increased IL-8 protein secreted to the medium (Figure 56D). Parental HUVEC endogenously expressed IL-8 protein in cell lysate and also secreted to the medium (Figure 57A). Additionally, exogenous rhTFF3 (at the lower concentration of rhTFF3 e.g., 0.1 and 1.0 ng/mL rhTFF3) marginally increased the expression of IL-8 mRNA (Figure 57B) and protein (Figure 57C) in parental HUVEC, suggesting that the lower concentration of exogenous rhTFF3 was able to stimulate IL-8 protein expression in parental HUVEC, albeit slightly.

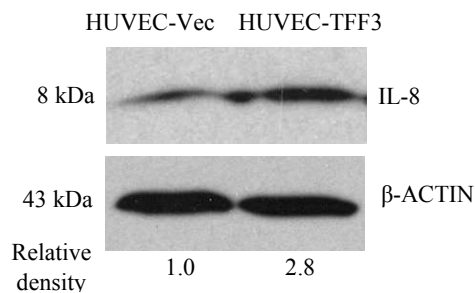
A RT-PCR



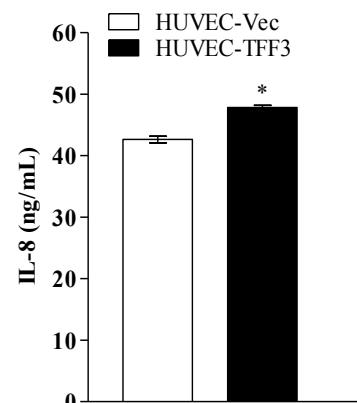
B RT-PCR



C Western blot



D ELISA



E RT-PCR

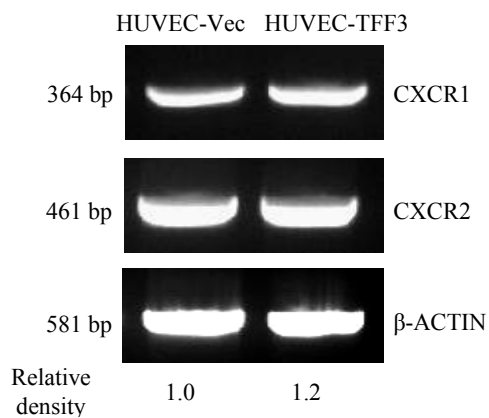


Figure 56: Forced expression of TFF3 in HUVEC increased IL-8 expression. A, semi-quantitative RT-PCR analysis of the expression of VEGF-A, VEGFR1, and VEGFR2 mRNA in HUVEC with forced expression of TFF3. HUVEC with empty vector was used as control. B, semi-quantitative RT-PCR analysis of IL-8 mRNA in HUVEC with forced expression of TFF3. C, Western blot analysis of IL-8 protein in HUVEC with forced expression of TFF3. D, ELISA analysis of IL-8 protein secreted to the medium by HUVEC with forced expression of TFF3. E, semi-quantitative RT-PCR analysis of the expression of IL-8 receptors, CXCR1 and CXCR2 mRNA in HUVEC with forced expression of TFF3. β-ACTIN was used as a loading control in semi-quantitative RT-PCR and Western blot analysis. *, $P < 0.05$.

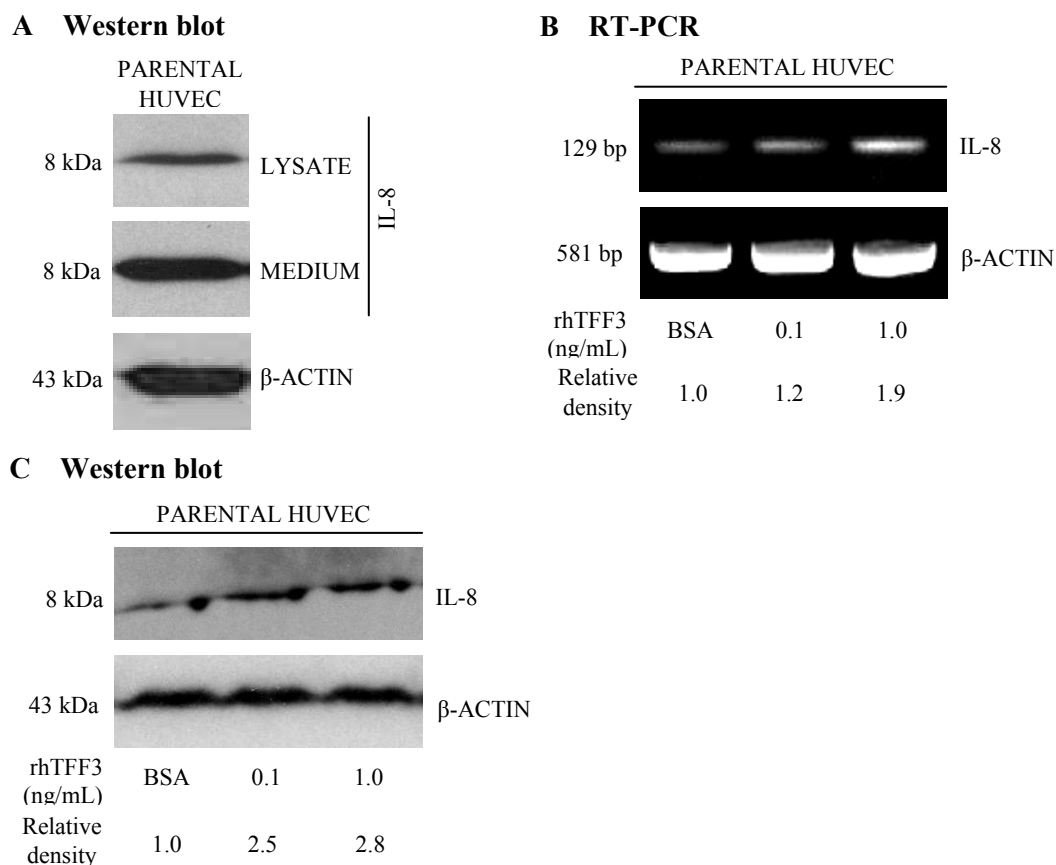


Figure 57: Exogenous rhTFF3 stimulation induced IL-8 expression in parental HUVEC. A, Western blot analysis of IL-8 protein in cell lysate and conditioned medium of Parental HUVEC. B, semi-quantitative RT-PCR analysis the expression of IL-8 mRNA in parental HUVEC treated with exogenous rhTFF3 (0.1, 1.0 ng/mL of rhTFF3) and BSA control. C, Western blot analysis of the expression of IL-8 protein in parental HUVEC treated with exogenous rhTFF3 (0.1, 1.0 ng/mL of rhTFF3) and BSA control. Parental HUVEC treated with BSA control was used as baseline. β-ACTIN was used as a loading control in semi-quantitative RT-PCR and Western blot analysis.

4.2.11 Depletion of TFF3 in HUVEC decreased IL-8 promoter activity and subsequently decreased IL-8 expression

I then determined if depletion of TFF3 in HUVEC decreased IL-8 promoter activity and subsequently its expression. Firstly, HUVEC with depletion of TFF3 was transiently transfected with full length of IL-8 promoter (-4800 to +104 bp). Depletion of TFF3 in HUVEC significantly lessened IL-8 promoter activity (2.3-fold decrease) when compared with the control HUVEC-siVec (Figure 58A). Secondly, HUVEC with depletion of TFF3 was transiently transfected with shorter IL-8 promoter, pGL-IL8-152 (-152 to + 44 bp). HUVEC

with depletion of TFF3 also lessened IL-8 promoter activity (1.9-fold decrease) when compared with the control HUVEC-siVec (Figure 58B). The transcription factors namely NF-IL-6, NF- κ B, and AP-1 present at the proximal region of IL-8 promoter are required for promoting of TFF3-stimulated IL-8 promoter activity in HUVEC. Furthermore, depletion of TFF3 in HUVEC by siRNA decreased IL-8 mRNA (Figure 58C) and IL-8 protein secreted to medium (Figure 58D) when compared with the control HUVEC-siVec. Hence, depletion of TFF3 by siRNA in HUVEC lessened the IL-8 promoter activity and subsequently decreased IL-8 expression in HUVEC.

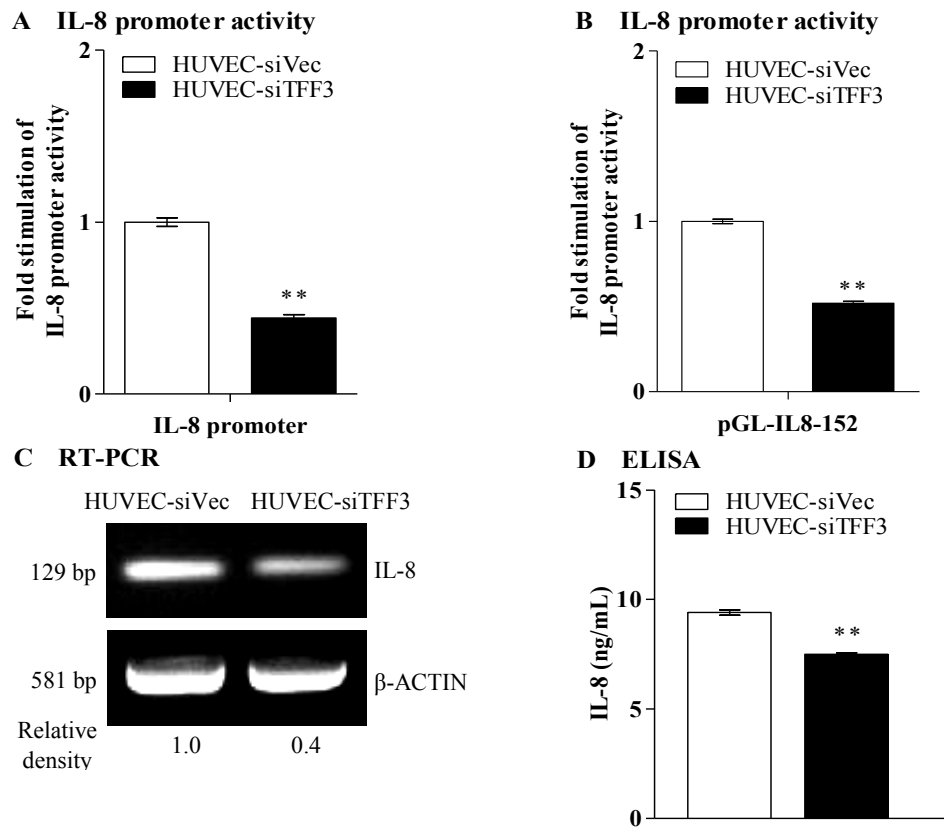


Figure 58: Depletion of TFF3 in HUVEC decreased IL-8 promoter activity and subsequently decreased IL-8 expression. A, IL-8 promoter activity in HUVEC with depletion of TFF3 transiently transfected with IL-8 promoter (full length, -4800 to + 104 bp). HUVEC with control siRNA was used as control. B, IL-8 promoter activity in HUVEC with depletion of TFF3 transiently transfected with pGL-IL8-152 reporter (-152 to +44 bp). HUVEC was transiently transfected with a reporter and a pRL-CMV control reporter. C, semi-quantitative RT-PCR analysis of IL-8 mRNA in HUVEC with depletion of TFF3. D, ELISA analysis of IL-8 protein secreted to the medium by HUVEC with depletion of TFF3. β -ACTIN was used as a loading control in semi-quantitative RT-PCR. **, $P < 0.01$.

4.3 Discussion

4.3.1 Exogenous rhTFF3 stimulation promoted angiogenic activity of HUVEC

Herein, I have demonstrated that exogenous rhTFF3 promoted HUVEC monolayer proliferation, migration, invasion, tubule formation *in vitro* in a concentration-dependent manner. Exogenous rhTFF3 directly acted on HUVEC to stimulate angiogenesis *in vitro*. Exogenous rhTFF3 stimulation increased HUVEC monolayer proliferation in 10% FBS conditions and induced a small increase of HUVEC monolayer proliferation in serum deprived conditions (0.2% FBS). Hence, exogenous rhTFF3 was able to stimulate HUVEC monolayer proliferation in both 10% FBS and serum deprived conditions. These results are supported by Kindon *et al.* (1995) who previously demonstrated that recombinant TFF3 protects human colon cancer cell monolayer from external insults. Protection of colon cancer cell from injury or damage was enhanced by the addition of both recombinant TFF3 and human colonic mucin (Kindon *et al.*, 1995). We have identified that TFF3 acted as mitogenic and cytoprotective factor.

All TFF peptides have been demonstrated to be motogenic and are involved in wound healing process by promotion of cell migration and resistance to anoikis. TFF3 and TFF1 are potent motogens in both normal and cancer cells. These peptides are able to promote migration of epithelial cells, TFF3 is the only family member that has been reported to be a crucial factor implicated in mucosa restitution (Mashimo *et al.*, 1996, Poulsom, 1996). Earlier studies have reported that exogenous rhTFF3 stimulated migration of intestinal epithelial cells *in vitro* (Dignass *et al.*, 1994, Chinery and Playford, 1995). Additionally, Taupin *et al.* (1999) showed that the migration rate of epidermal cells was significantly increased after rhTFF3 treatment. Furthermore, Li *et al.* (2011) recently demonstrated that rhTFF3 slightly increased the expression of EGF, enhanced the restitution of the damaged mucosa and increased migration of the epithelial cells, thus promoting the healing of injured mucosa in colitis (Li *et al.*, 2011). Concordantly, I have demonstrated that exogenous rhTFF3 may function as both chemoattractant and stimulant to promote migration of endothelial cells but more remarkable

as a chemoattractant. I suggested that TFF3 is a potent chemotactic factor for endothelial cells and stimulates directional movement of endothelial cells towards increasing concentration of rhTFF3. I have also shown that exogenous rhTFF3 promoted HUVEC migration and invasion in a concentration-dependent manner with maximal stimulation at 5.0 ng/mL rhTFF3. Exogenous rhTFF3 is able to stimulate HUVEC migration and invasion. Notably, the effect of exogenous rhTFF3 on HUVEC migration was more prominent than invasion. Similarly, exogenous rhTFF1 stimulates migration and proliferation of mammary carcinoma cells (May and Westley, 1997a, Prest *et al.*, 2002). Prest *et al.* (2002) has suggested that rhTFF1 may stimulate cell migration by interacting with cell surface receptors. After mucosal injury, a functional EGF receptor is required for activation of TFF gene transcription through the Ras/MEK/MAP kinase signaling pathway (Taupin *et al.*, 1999). Since activation of MAP kinase enhanced cell migration, the effects of trefoil peptides on epithelial restitution may occur through MAP kinase signaling pathway (Taupin *et al.*, 1999). TFF peptides indirectly activated EGF-R to stimulate the TFF-mediated signaling events (McKenzie *et al.*, 1997, Taupin *et al.*, 1999). TFF peptides and EGF have been reported to exert synergistic effects in promotion of cell migration (Poulsom, 1996). However, TFF3 stimulates cell invasion through an EGFR-independent signaling pathway (Rodrigues *et al.*, 2003b). TFF3 induced intestinal epithelial cells resistance to apoptosis via activation of nuclear factor- κ B (NF- κ B), a pivotal regulator implicated in survival pathway of intestinal epithelial cells. Hence, intestinal epithelial cells treated with recombinant TFF3 were resistant to anoikis (Chen *et al.*, 2000). The anti-apoptotic function of TFF3 in colon cancer was regulated via an alternative signaling cascade such as PI3K, protein kinase B (PKB), and NF- κ B. Blocking of EGF signaling abrogated TFF3-stimulated cell survival and partially inhibited Erk/MAPK-dependent transcriptional signaling following TFF3 stimulation (Taupin *et al.*, 1999). These observations suggested that TFF peptides stimulated activation of Erk/MAPK through alternative pathways.

Addition of exogenous recombinant human TFF1 and TFF3 has been reported to promote formation of capillary vessel in a CAM assay. Exogenous rhTFF1 stimulated

HUVEC to form tubules in the Matrigel and the angiogenic activity of rhTFF1 is comparable to that stimulated by VEGF-A and TGF- α (Rodrigues *et al.*, 2003b). Since TFF3 is analogous with TFF1, TFF3 may also function as pro-angiogenic factor to promote angiogenesis *in vivo*. Concordant with these observations, I have demonstrated that exogenous rhTFF3 directly acted on endothelial cells and promoted tubule formation *in vitro* in a concentration-dependent manner with the maximal stimulation at 5.0 ng/mL rhTFF3. Notably, higher concentrations of exogenous rhTFF3 (10 ng/mL rhTFF3) exerted lesser stimulatory effect on HUVEC tubule formation *in vitro*. Previous reports have demonstrated that 100 nM of recombinant TFF1 and TFF3 were needed to stimulate capillary vessel formation in CAM assay or tubule formation *in vitro* (Rodrigues *et al.*, 2003b). Additionally, migration of MCF-7 cell lines was stimulated by 10 μ g/mL of recombinant TFF1 (Prest *et al.*, 2002). In relation to this observation, Prest *et al.*, (2002) proposed that TFF1 and possibly TFF3, at the higher concentrations may inhibit dimerization of the putative TFF receptor and subsequently lead to attenuation of receptor activation for signal transduction. Angiogenesis *in vitro* induced by TFF peptides was demonstrated to be dependent on both cyclooxygenase (COX-2) and the EGF-R tyrosine kinase to mediate pro-angiogenic activity of TFF3 (Rodrigues *et al.*, 2001). Increased expression of COX-2 promotes resistance to apoptosis and tumor angiogenesis as well as enhances invasion and metastasis (Labayle *et al.*, 1991, Jacoby *et al.*, 1996, Tsujii *et al.*, 1998). Furthermore, nitric oxide plays an important role in tumor angiogenesis, and TFF3 has been demonstrated to enhance nitric oxide (NO) formation through the inducible nitric oxide synthase (iNOS/NOS2) (Tan *et al.*, 1999).

Although TFF1 and TFF3 peptides only contain a single trefoil domain, they are capable of forming homodimers via utilization of an unpaired cysteine residue located near the C-terminus (May *et al.*, 2003). TFF1 dimer is more potent in stimulating migration of mammary carcinoma cells via a bivalent dimeric receptor (Marchbank *et al.*, 1998, Prest *et al.*, 2002). Additionally, TFF1 dimer is more biologically active than TFF1 monomer in preventing drug-induced gastric damage and promoting cell migration. It has been postulated

that dimerization may enhance the interaction of TFF1 with its receptor (Marchbank *et al.*, 1998). The relative biological activity of dimeric and monomeric recombinant TFF3 has been compared in a mice model of ischaemic necrotising enterocolitis. TFF3 dimer was shown to possess a similar potency as the TFF3 monomer and both forms of recombinant TFF3 promoted healing of intestinal injury induced by ischemia (Carrasco *et al.*, 2004). It has been suggested that TFF3 dimer is necessary for activation of signal transduction pathways in intestinal epithelial cells, for instance PI3K and NF- κ B survival pathways (Taupin *et al.*, 1999).

The combined functions of TFF peptides and mucin may cooperatively protect the mucosa from injury and increase mucus viscosity (Kindon *et al.*, 1995). The interaction between TFF peptide and mucin has also been demonstrated to enhance cell migration and nitric oxide production (Dignass *et al.*, 1994, Tan *et al.*, 1999). TFF1 is co-localized with MUC5AC and TFF3 is co-localized with MUC2 in the gastrointestinal tract, indicating that specific TFF peptides may have specific mucin partner (Longman *et al.*, 2000). Moreover, Chinery and Cox (1995) have suggested that TFF3 binds to a phosphorylated tyrosine-containing peptide of 28 kDa. Recent evidence has reported that mutation in the brichos domain of SP-C promoted annexin V association and subsequent apoptosis by activating caspase 3 (Mulugeta *et al.*, 2005), suggesting that there was a putative binding between trefoil factors and the brichos domain, which can abrogate anti-apoptotic activity of TFF3 (Mulugeta *et al.*, 2005). Many reports pertaining to the functions of trefoil factors are suggestive of a receptor-mediated mode of action such as activation of tyrosine kinase or tyrosine phosphatase, and signaling via transduction pathways such as RAS/MEK/MAPK (Kanai *et al.*, 1998, Taupin *et al.*, 1999). However, there is still no trefoil factors binding molecule with the canonical characteristics of a receptor that has yet been identified (Otto and Thim, 2005). A recent study suggested TFF3 receptor is present in the intestinal epithelial cells and the binding between this receptor and TFF3 is as if specific receptor-ligand interaction. The

identity of this specific TFF3 receptor is yet to be identified and required for further investigation (Yong *et al.*, 2013).

In summary, exogenous rhTFF3 can directly stimulate angiogenic behaviors of endothelial cells, although HUVEC endogenously expressed relatively low level of TFF3. Hence, exogenous rhTFF3 is able to stimulate angiogenesis *in vitro*.

4.3.2 Forced expression of TFF3 in HUVEC promoted angiogenesis

I have demonstrated that forced expression of TFF3 in HUVEC promoted angiogenic behavior of endothelial cells through an autocrine loop. Additionally, TFF3 secreted from HUVEC may exhibit similar functions as exogenous rhTFF3 stimulation and thus stimulated angiogenic behaviors of endothelial cells. The effect of forced expression of TFF3 in HUVEC was generally not very drastic because the function of TFF3 in endothelial cells is more predisposed in maintaining the angiogenic activity and normal cellular processes (Kinoshita *et al.*, 2000a, Podolsky, 2000, Taupin *et al.*, 2000a). The ability of TFF3 to stimulate angiogenic behaviors of endothelial cells was consistent with others secreted protein such as Artemin secreted from mammary carcinoma cells that exhibited its stimulatory effect on HMEC-1 around 20 - 30% (Banerjee *et al.*, 2011). Endothelial cells expressed undetectable or very low level of TFF3 (Dhar *et al.*, 2005, Kjellef, 2009). Concordantly, HUVEC utilized in this study also expressed undetectable or very low level of TFF3 protein. Forced expression of TFF3 in HUVEC promoted monolayer cell proliferation, cell cycle progression, survival, migration, invasion, and tubule formation *in vitro*. Depletion of TFF3 by siRNA in HUVEC decreased angiogenic behaviors of endothelial cells. In general, increased TFF3 expression in HUVEC exhibited lesser effect in cellular processes than exogenous rhTFF3 stimulation.

The mitogenic role of TFF3 in normal and cancer cells are controversial. Over-expression of TFF3 has been reported to decrease cell proliferation of human gastrointestinal cells (Uchino *et al.*, 2000, Bossenmeyer-Pourie *et al.*, 2002). In contrast, increased TFF3

expression in mammary carcinoma cells promoted cell proliferation (Xu *et al.*, 2005, Kannan *et al.*, 2010). I have demonstrated that TFF3 secreted from HUVEC promoted monolayer cell proliferation by increased cell cycle progression and decreased apoptotic cell death, suggesting that TFF3 secreted from HUVEC may act as pro-mitogenic and pro-survival factor. Concordantly, TFF3 was shown to protect intestinal epithelial cells from apoptosis after mucosal damage is dependent on PI3K and EGF-R signaling pathways. Additionally, TFF3 also promotes serine phosphorylation of Akt kinase, which is associated with cell survival (Kinoshita *et al.*, 2000b, Podolsky, 2000, Taupin *et al.*, 2000b).

It is well established that TFF3 promotes intestinal epithelial cell migration and resistance to apoptosis in the process of mucosa restitution (Dignass *et al.*, 1994, Playford *et al.*, 1995). The pro-migratory function of TFF3 has furthermore been observed in epithelial cells not from the gastrointestinal tract, suggesting that TFF peptides are normally expressed in any type of epithelial cells and its functions are cell-type specific (Kjellev, 2009). TFF3 is an anti-apoptotic protein secreted by goblet cells to protect intestinal epithelial cells from anoikis (Regalo *et al.*, 2005). It has been shown that TFF3 stimulated intestinal epithelial cell resistance to anoikis via activation of NF- κ B signaling pathway (Chen *et al.*, 2000). Another study has reported that TFF3 exerted anti-anoikis effects on the intestinal cells through activation of EGF-R signaling pathway (Kinoshita *et al.*, 2000a). Consistent with these previous reports, I have demonstrated that TFF3 secreted from HUVEC promoted cell migration, invasion and tubule formation *in vitro*, supporting that TFF3 enhanced angiogenic behaviors of HUVEC to promote angiogenesis *in vitro*. Similarly, TFF3 secreted from mammary carcinoma cells also was able to stimulate angiogenic behaviors of HUVEC and promoted *de novo* angiogenesis in mammary carcinoma via STAT3/IL-8 dependent signaling pathway.

Cancer cells often lose cadherin function in the transition to an invasive and metastatic phenotype (Perl *et al.*, 1998, Cavallaro *et al.*, 2002). Experimental evidence has suggested that TFF3 promoted cell migration requires modulation of E-cadherin function and

tyrosine phosphorylation of β -catenins (Liu *et al.*, 1997, Efstathiou *et al.*, 1998, Efstathiou *et al.*, 1999). TFF3 stimulated migration and invasion of rat fibroblastic cells that correlated with down-regulated E-cadherin and tissue inhibitor of metalloproteinase-1 (TIMP-1) as well as increased β -catenin and metalloproteinase-9 (MMP-9) (Chan *et al.*, 2005b). TFF3 has also been shown to promote colon cancer cell migration through repression of E-cadherin-catenin complex formation (Emami *et al.*, 2004). Additionally, TFF3 promoted migration of both normal and oncogenically transformed bronchial epithelial cells through activation of MAPK pathway (Graness *et al.*, 2002). Collectively, TFF3 may also promote cell migration of endothelial and mammary carcinoma cells through the same signaling pathways.

In the past decades, numerous of angiogenic factors have been reported that can promote both differentiation and proliferation of endothelial cells. Of these angiogenic factors, VEGF-A and IL-8 are the most potent regulators of tumor angiogenesis (Koch *et al.*, 1992, Nor *et al.*, 1999). VEGF-A is also known as an endothelial-cell-specific mitogen and vascular permeability factor that promotes *de novo* angiogenesis (Nor *et al.*, 1999). Nevertheless, I have observed that TFF3 secreted from HUVEC may not able to stimulate the expression of VEGF-A and its receptors, indicating that VEGF-A was probably not involved in TFF3-stimulated tumor angiogenesis. Another potent angiogenic factor, IL-8 is synthesized in multiple different cell types including cancer and endothelial cells (Polverini, 1995, Strieter *et al.*, 1995b). IL-8 binds to its cognate receptors to mediate endothelial proliferation, survival and tumor angiogenesis (Rollins, 1997, Addison *et al.*, 2000). It has been reported that CXCR1 and CXCR2 are expressed in endothelial cells and thus IL-8 interacts with endothelial cells through these receptors and induces tumor angiogenesis (Murdoch *et al.*, 1999, Addison *et al.*, 2000, Salcedo *et al.*, 2000b). Consistent with these reports, I have demonstrated that TFF3 secreted from HUVEC slightly increased IL-8 expression. Parental HUVEC endogenously expressed IL-8 but its expression was also marginally increased in response to exogenous TFF3 stimulation. Both CXCR1 and CXCR2 mRNAs were present in HUVEC with forced expression of TFF3.

Increased the expression of IL-8 has been characterized in cancer cells and endothelial cells. IL-8 has the capacity to exert oncogenic effects in the tumor microenvironment. For example, secretion of IL-8 can activate endothelial cells in the tumor vasculature to promote angiogenesis (Oude Nijhuis *et al.*, 2003, Ramjeesingh *et al.*, 2003, Vadeboncoeur *et al.*, 2003). Previous reports have highlighted that IL-8 promoter activity appears to be regulated by the combinatorial activation and binding of NF- κ B, NF-IL-6, and AP-1 families of transcription factors (Mukaida *et al.*, 1990, Roebuck, 1999). I have observed that TFF3 secreted from HUVEC stimulated IL-8 promoter activity and subsequently lead to a slight increase of IL-8 expression. Additionally, the transcription factors namely NF- κ B, NF-IL-6, and AP-1 are required for promoting TFF3-stimulated IL-8 promoter activity in HUVEC.

In summary, TFF3 secreted from endothelial cells promoted monolayer proliferation, cell cycle progression, survival, migration, invasion and tubule formation *in vitro*. Depletion of TFF3 in HUVEC diminished the ability of TFF3 on stimulation of angiogenic behaviors of endothelial cells. TFF3 secreted from HUVEC stimulated angiogenic behaviors of endothelial cells through an autocrine manner.

CHAPTER 5

General Conclusion and Future Direction

5.1 General conclusion

5.1.1 TFF3 promoted *de novo* angiogenesis in mammary carcinoma

The main focus of this study was to investigate the role of TFF3 in promoting *de novo* angiogenesis in mammary carcinoma and delineate the underlying mechanism by which TFF3 may exert this effect. Herein, I have demonstrated that TFF3 secreted either from mammary carcinoma cells or HUVEC stimulated angiogenic behaviors of endothelial cells and thus promote *de novo* angiogenesis. TFF3 secreted from mammary carcinoma cells exhibited more compelling effect on stimulation of angiogenic behaviors of endothelial cells when compared with the autonomous effect of TFF3 in HUVEC. TFF3 has been shown to promote survival, invasion, and metastatic expansion of mammary carcinoma (Kannan *et al.*, 2010, Ahmed *et al.*, 2012, Pandey *et al.*, 2014). In addition to other growth factors produced by mammary carcinoma cells (Perry *et al.*, 2008), TFF3 was able to stimulate angiogenic behaviors of endothelial cells. In contrast, the autonomous effect of TFF3 in HUVEC was generally not very drastic because the role of TFF3 in endothelial cells is more predisposed in maintaining angiogenic activity and normal cellular processes (Kinoshita *et al.*, 2000a, Podolsky, 2000, Taupin *et al.*, 2000a). It is known that the functions of TFF3 are cell-type specific, for instance, TFF3 normally expressed in gastric mucosa and is involved in protection of GI tract against mucosal damage (Taupin and Podolsky, 2003, Hoffmann, 2006), however increased TFF3 expression promotes tumorigenesis of mammary carcinoma (Kannan *et al.*, 2010, Ahmed *et al.*, 2012, Pandey *et al.*, 2014).

I have demonstrated that TFF3 secreted from mammary carcinoma cells stimulated HUVEC monolayer proliferation, cell cycle progression, survival, migration, invasion, and tubule formation *in vitro*. Depletion of TFF3 in mammary carcinoma cells by siRNA diminished HUVEC monolayer proliferation, cell cycle progression, survival, migration,

invasion and tubule formation *in vitro*. In a xenograft model, forced expression of TFF3 in MCF-7 cells produced tumors with increased IL-8 protein expression and enhanced microvessel density (as indicated by increased area of both CD31- and CD34-labeled cells) when compared with tumors produced by control MCF7-Vec cells. These observations further confirmed that TFF3 promotes tumor angiogenesis *in vivo*.

Tumor angiogenesis is modulated by a large number of secreted angiogenic proteins (Sudhakar, 2009). I therefore examined a range of angiogenic factors implicated in angiogenesis and observed that TFF3 regulated the gene expression of IL-8. Increased TFF3 expression in mammary carcinoma cells promoted IL-8 expression. The functional roles of IL-8 in promotion of invasion, survival and chemotherapeutic drug resistance of prostate cancer cell lines could be effectively inhibited by IL-8 siRNA (Singh and Lokeshwar, 2009). Hence, I employed the same IL-8 siRNA to selectively deplete IL-8 expression in MCF-7 cells with forced expression of TFF3. TFF3 secreted from mammary carcinoma cells stimulated IL-8 promoter activity and subsequently increased the expression of IL-8. Depletion of IL-8 by siRNA in mammary carcinoma cells with forced expression of TFF3 decreased IL-8 protein expression. Depletion of IL-8 by siRNA in mammary carcinoma cells significantly abrogated the stimulatory effect of TFF3 on HUVEC migration, invasion and tubule formation *in vitro*. It has been reported that neutralizing antibodies to IL-8, CXCR1 or CXCR2 abrogated endothelial cell proliferation, survival, migration, and angiogenesis as compared to control antibody (Li *et al.*, 2005). Therefore, I utilized the same clone of anti-IL-8 monoclonal antibody inhibitory to TFF3 on stimulation of angiogenic behaviors of endothelial cells mediated by IL-8. Blocking of IL-8 in mammary carcinoma cells by anti-IL-8 monoclonal antibody inhibited the ability of TFF3 on stimulation of HUVEC tubule formation *in vitro*. These results suggested that depletion of IL-8 in mammary carcinoma cells by siRNA or inhibition of IL-8 with anti-IL-8 monoclonal antibody abrogated the ability of TFF3 to stimulate the angiogenic behaviors of endothelial cells. Additionally, blocking of CXCR1 in HUVEC by anti-CXCR1 monoclonal antibody may not be able to inhibit the

stimulatory effect of TFF3 on HUVEC tubule formation *in vitro*. However, blocking of CXCR2 in HUVEC by use of anti-CXCR2 monoclonal antibody inhibited the stimulatory effect of TFF3 on HUVEC tubule formation *in vitro* mediated by IL-8. It is known that CXCR2 receptor has other ligands such as IL-1, IL-2 and IL-6 (Addison *et al.*, 2000). It is possible that anti-CXCR2 is disrupting IL-8 independent events. Hence, the ability of TFF3 to stimulate angiogenic behaviors of endothelial cells was mediated by IL-8/CXCR2 axis.

IL-8 is synthesized in different cells in response to inflammatory stimuli such as that provided by IL-1 and TNF- α (Brasier *et al.*, 1998). Up-regulation of IL-8 gene expression is achieved through activation of NF- κ B in concert with other transcription factors and also dependent on cell type and stimuli (Mukaida *et al.*, 1994). IL-8 promoter contains response elements for a number of different transcription factors and has been reported to constitute with pro-inflammatory responsive elements important for IL-8 gene expression (Mukaida *et al.*, 1989, Mukaida *et al.*, 1994). Several studies have suggested that production of IL-8 protein is regulated by STAT3 through direct binding to consensus binding site at the proximal region of IL-8 promoter gene (Seidel *et al.*, 1995, Oka *et al.*, 2010).

Herein, I have demonstrated that the transcription factors namely AP-1, NF-IL-6, and NF- κ B at the proximal region of IL-8 promoter were necessary for enhancing IL-8 promoter activity stimulated by TFF3. In fact, the expression of IL-8 is regulated by multiple transcription factors. Besides these transcription factors, TFF3 secreted from mammary carcinoma cells activated and increased tyrosine phosphorylation of STAT3. Depletion of STAT3 by siRNA partially abrogated the effect of TFF3 on IL-8 promoter activity and resulted in a small decrease of IL-8 expression. Hence, I postulate that STAT3 is one of a number of factors involved in the regulation of IL-8 expression stimulated by TFF3. Presumably, STAT3 is a transcription factor for IL-8 and cooperate with other transcription factors in the regulation of IL-8. TFF3 secreted from mammary carcinoma cells stimulated tyrosine phosphorylation of STAT3, the activated STAT3 dimerizes, and translocates into the nucleus to activate IL-8 gene expression (Bromberg *et al.*, 1999, Niu *et al.*, 2002, Rivat *et al.*,

2005). It has been reported that IL-6 induced STAT3 phosphorylation and increased the expression of TFF3 to promote cell migration and wound healing in biliary epithelial cells, which is through the activation of STAT3 and subsequent up-regulation of TFF3 expression (Jiang *et al.*, 2010). Additionally, TFF3 and VEGF-A function as promoters of colon cancer cell invasion, survival, and angiogenesis through STAT3-dependent signaling pathway (Rivat *et al.*, 2005). Earlier studies reported that VEGF-A activates STAT3, which in turn increased VEGF-A gene expression (Niu *et al.*, 1999, Niu *et al.*, 2002). It has been reported that TFF3 activated STAT3 activity to promote TFF3 gene transcription via autocrine loop (Rivat *et al.*, 2005). TFF3 and VEGFA have been demonstrated to activate STAT3 through tyrosine (Y705) phosphorylation of STAT3- α and STAT3- β isoforms (Bromberg *et al.*, 1999). TFF3 and VEGFA promoted cellular invasion and migration of colon cancer cells (Rivat *et al.*, 2005). Notably, TFF1 does not promote activation of STAT3, yet TFF1 was still capable to promote cellular invasion (Rivat *et al.*, 2005). Recently, TFF3 has been shown to promote invasion and metastasis of mammary carcinoma cells in Src-STAT3 dependent manner (Pandey *et al.*, 2014).

The constitutively active STAT3 increases VEGF-A expression and induces tumor angiogenesis in human pancreatic cancer cells. However, inhibition of STAT3 signaling with dominant-negative STAT3 inhibits VEGF-A expression, angiogenesis, and tumor growth (Wei *et al.*, 2003a). IL-6 stimulated VEGF-A protein expression in cervical cancer cells through activation of STAT3 phosphorylation. However, abrogation of the STAT3 pathway with a dominant-negative STAT3 protein reduced IL-6 stimulated tumor angiogenesis and the growth of cervical cancer cells (Wei *et al.*, 2003b). In accordance with these evidences, I have shown that STAT3 partially mediated the action of TFF3 on the stimulation of angiogenic behaviors of endothelial cells. Depletion of STAT3 by siRNA in mammary carcinoma cells with forced expression of TFF3 partially abrogated the effect of TFF3 on HUVEC migration, invasion and tubule formation *in vitro*. Mechanistically, TFF3 increased IL-8 expression and STAT3 phosphorylation that can partially elevated the expression of IL-8, which in turn

mediated the ability of TFF3 on the stimulation of angiogenic behaviors of endothelial cells via IL-8/CXCR2 axis. Therefore, TFF3 is a promoter of angiogenesis, which may also co-coordinate with the growth promoting and metastatic actions of TFF3 in mammary carcinoma to enhance tumor progression (Figure 59).

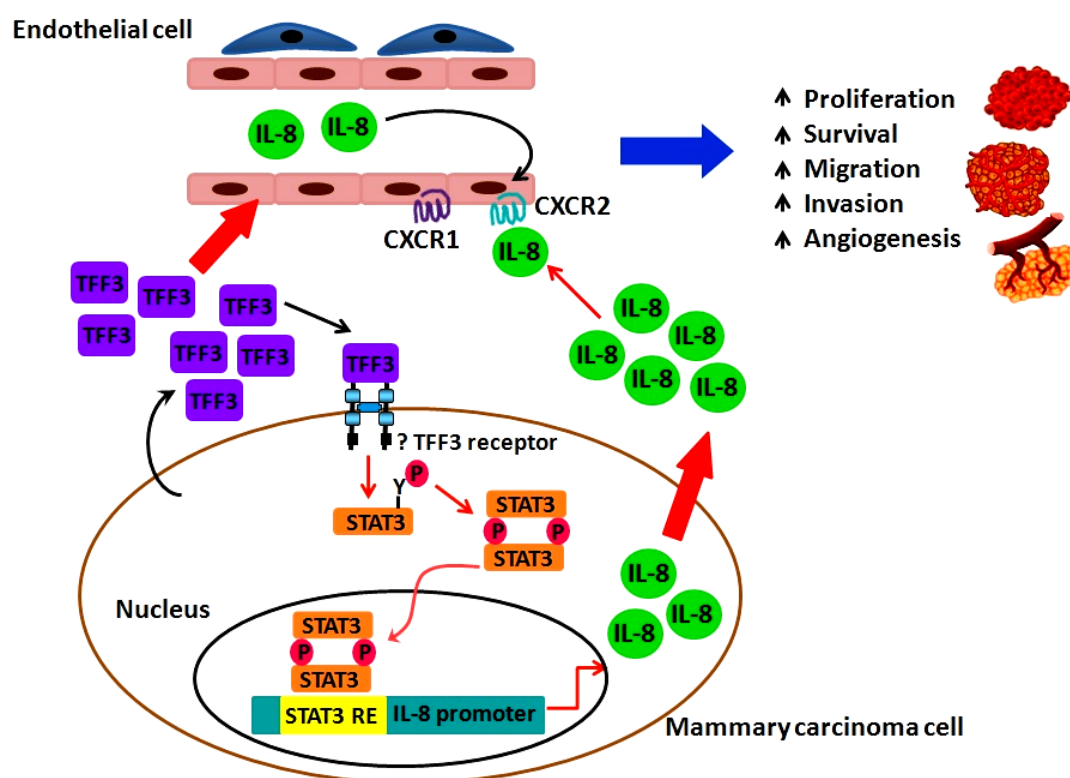


Figure 59: TFF3 is a promoter of angiogenesis in mammary carcinoma. TFF3 promoted IL-8 expression and increased tyrosine phosphorylation of STAT3 that is partially involved in the regulation of IL-8. The ability of TFF3 to stimulate angiogenic behaviors of HUVEC was mediated by IL-8 through CXCR2 axis. Furthermore, exogenous rhTFF3 directly acted on HUVEC to promote angiogenic behaviors of HUVEC. Additionally, TFF3 secreted from HUVEC promoted angiogenesis *in vitro* mediated by IL-8. Therefore, TFF3 is a promoter of angiogenesis, which may also co-coordinate with the growth promoting and metastatic actions of TFF3 in mammary carcinoma to enhance tumor progression.

In summary, I have demonstrated that depletion of TFF3 by siRNA in mammary carcinoma cells diminished the angiogenic behaviors of HUVEC. A previous study has reported that neutralization of TFF3 by anti-TFF3 polyclonal antibody reduced cell viability of mammary carcinoma cells and inhibited tumor growth in xenograft models (Kannan *et al.*, 2010). Collectively, inhibition of TFF3 by siRNA or anti-TFF3 antibody can be an effective

strategy to suppress tumor angiogenesis and metastasis in mammary carcinoma. Depletion of IL-8 by siRNA and inhibition IL-8 with anti-IL-8 monoclonal antibody abrogated the ability of TFF3 to stimulate angiogenic behaviors of HUVEC mediated by IL-8. Consistently, human anti-IL-8 antibody (e.g., ABX-IL8) has been reported to inhibit tumor angiogenesis, growth, and metastasis in bladder cancer and melanoma (Yang *et al.*, 1999, Huang *et al.*, 2002, Mian *et al.*, 2003). In addition, preclinical evaluation of the effectiveness of repertaxin (inhibitor of CXCR1/2) on animal models showed that mice treated with repertaxin developed fewer metastases than the mice treated with chemotherapy alone (Ginestier *et al.*, 2010). Therefore, the functional antagonism of TFF3 and/or IL-8 in mammary carcinoma cells could be a promising therapeutic strategy for suppression of the growth of TFF3-stimulated carcinomas.

5.5.2 Exogenous rhTFF3 stimulation and TFF3 secreted from HUVEC promoted angiogenesis

Herein, I have demonstrated that exogenous rhTFF3 stimulated HUVEC monolayer proliferation, migration, invasion, and tubule formation *in vitro* in concentration-dependent manner. Exogenous rhTFF3 directly acted on HUVEC to promote angiogenesis *in vitro*. Exogenous rhTFF3 may serve as both chemoattractant and stimulant to promote HUVEC migration and invasion. I suggested that TFF3 is a pro-angiogenic factor to promote angiogenic behaviors of endothelial cells through an autocrine loop. The angiogenic responsiveness of endothelial cells to the stimulation of TFF3 reflects the functional roles of TFF3 are unique, cell-type specific and implicated in different tissue of origin.

TFF3 secreted from HUVEC promoted monolayer cell proliferation, cell cycle progression, survival, migration, invasion, tubule formation *in vitro*. Depletion of TFF3 by siRNA in HUVEC decreased angiogenic behaviors of endothelial cells. TFF3 secreted from HUVEC exhibited similar functional effects as exogenous rhTFF3 stimulation. The protein expression of IL-8 in HUVEC was marginally increased by exogenous rhTFF3 stimulation. Additionally, TFF3 secreted from HUVEC was able to stimulate IL-8 promoter activity and

subsequently increased IL-8 expression, which in turn mediated the action of TFF3 to promote angiogenesis *in vitro* (Figure 59).

Considering therapeutic implications, both TFF3 siRNA and anti-sense TFF3 suppressed the growth and tumorigenicity of mammary carcinoma (Kannan *et al.*, 2010). The anti-tumorigenic effect is mediated through induction of apoptosis and restored tamoxifen sensitivity in tamoxifen-resistance mammary carcinoma cells (Kannan *et al.*, 2010). TFF3 protein expression in tamoxifen-resistance mammary carcinoma cells was substantially increased and further induced by tamoxifen. Functional antagonism of TFF3 by antibody inhibited cell growth and improved tamoxifen sensitivity of tamoxifen-resistance mammary carcinoma cells (Kannan *et al.*, 2010). Over-expression of IL-8 is associated with a drug resistance phenotype (Duan *et al.*, 1999). Hence, neutralizing antibody IL-8 reversed the drug-resistance of MCF-7 cells to a taxol and doxorubicin. Inhibition of endogenous IL-8 by siRNA significantly enhanced the drug sensitivity of the drug resistant MCF-7 cells (Shi *et al.*, 2012). Additionally, depletion of IL-8 in prostate cancer increased the cytotoxic potency of a number of chemotherapeutic drugs (Singh and Lokeshwar, 2009). Therefore, anti-IL-8 antibody not only inhibit endothelial cell proliferation and capillary tube formation, but this neutralizing antibody also can restore the drug sensitivity of the doxorubicin resistant MCF-7 cells (Li *et al.*, 2005, Shi *et al.*, 2012). Hence, the functional antagonism of TFF3 and IL-8 would be an effective therapeutic approach to abolish the ability of TFF3 on the stimulation of *de novo* angiogenesis in mammary carcinoma.

5.2 Future direction

TFF3 is a small secreted protein and amenable to inhibition by antibody, inhibitor, and RNAi molecule. Several studies have attempted to delineate the potential of TFF3 antagonism as a cancer therapeutic. One study has recently employed anti-TFF3 polyclonal antibody to neutralize the secreted TFF3 from mammary carcinoma cells. Neutralization of TFF3 by anti-TFF3 polyclonal antibody reduced cell viability of mammary carcinoma cells and inhibited xenograft growth (Kannan *et al.*, 2010). The anti-TFF3 polyclonal antibody exhibited no potential adverse effects on the vital organs including liver, lung, intestine, kidney, and stomach in mice treated with anti-TFF3 polyclonal antibody when compared with mice treated with Ig-G control. Additionally, it has been reported that anti-sense TFF3 molecule inhibits the growth of gastric cancer cells, increases adriamycin-induced apoptosis, and enhances the response to chemotherapy (Chan *et al.*, 2005a). The anti-TFF3 polyclonal antibody and anti-sense TFF3 molecule can be utilized for studying the functional antagonism of TFF3 for suppression of *de novo* angiogenesis in mammary carcinoma. Alternatively, it is worth to develop inhibitor of TFF3 or neutralizing agent comprises RNAi molecule that can specifically target to TFF3 functional domain.

The effect of inhibition of TFF3 in mammary carcinoma cells by anti-TFF3 polyclonal antibody or inhibitor of TFF3 on the angiogenic activity of endothelial cells is required for further investigation. The *in vitro* functional antagonism study may define the effectiveness of anti-TFF3 polyclonal antibody to abrogate the effect of TFF3 in *de novo* angiogenesis in mammary carcinoma. The xenograft study may provide *in vivo* evidence to support that the functional antagonism of TFF3 by anti-TFF3 polyclonal antibody is capable to suppress tumor angiogenesis and metastasis of mammary carcinoma. This approach may be a novel therapeutic strategy for treatment of tumor angiogenesis stimulated by TFF3 in mammary carcinoma and it may also applicable for other neoplastic disorders. The efficacy, safety, and route of administration of TFF3 neutralizing agent or inhibitor of TFF3 are

required for further investigation and this agent may be of value in pharmacological intervention (Kjellev, 2009).

I have also demonstrated that TFF3 stimulated activation of STAT3 phosphorylation in mammary carcinoma cells. STAT3 partially increased the expression of IL-8 and partially mediated the effect of TFF3 on stimulation of angiogenic behaviors of endothelial cells. STAT3 is one of a number of transcription factors involved in the regulation of IL-8 expression. The mechanism by which TFF3 stimulated the activation of STAT3 in the regulation of IL-8 expression remains unclear. A study has reported that STAT3 may directly bind to the IL-8 promoter gene in the region from -272 to -133 bp (Oka *et al.*, 2010). A potential STAT3-binding sequence TTCACCAAA, consistent with the reported consensus sequences TT(N₄/N₅)AA, was identified from -245 to -237 bp in the 5'-flanking region of the IL-8 gene (Seidel *et al.*, 1995). Thereby, I propose that TFF3 stimulates activation of STAT3 and mediates direct binding of STAT3 to its consensus sites in IL-8 promoter. The potential STAT3-binding sites in IL-8 promoter would be validated by searching the 5'-flanking region of IL-8 gene for consensus STAT3-binding sites, TT(N₄)AA and TT(N₅)AA (Seidel *et al.*, 1995) using DNASTar sequence analysis software. The putative STAT3-binding site from -245 to -237 bp in the 5'-flanking region of human IL-8 gene cloned into the luciferase reporter plasmid pGL3-Basic and designated as wild-type construct. The mutation of individual base pairs in plasmid DNA (from 5'-TTCCCAAA-3' to 5'-GCGTCAAA-3') can be constructed according to site-specific mutagenesis procedure (Deng and Nickoloff, 1992) or using Site-Directed Mutagenesis Kit. The STAT3 mutant can be confirmed by sequencing. IL-8 promoter activity for STAT3 mutant will be assayed to determine if STAT3 is involved in the regulation of IL-8 expression stimulated by TFF3 and if STAT3 is one of the transcription factors required for activation of IL-8 expression. Furthermore, chromatin immunoprecipitation (ChIP) assays will be performed to determine if STAT3 directly bind to the STAT3-binding site in the IL-8 promoter *in vivo*. ChIP assay is commonly used for the identification of particular genomic DNA sequences that associated with a specific

transcription factor (Wells *et al.*, 2000). Thereby, the ChIP assay will validate if STAT3 directly bind to its consensus-binding site at the IL-8 promoter mediated by TFF3, IL-8 is the target gene of STAT3, and STAT3 is a transcription factor for IL-8. The other transcription factors for example, interferon regulatory factor-1 in the IL-8 promoter gene may be involved in the regulation of IL-8 mediated by TFF3 and these factors can be examined by the same approach.

The major challenge of future work is to identify the receptor(s) for TFF3 to mediate its functional effects in promoting of tumor growth and metastasis of cancers. Although a few of TFF3-binding proteins have recently been characterized, the receptor that mediates TFF3 signaling has not yet been identified (Otto and Thim, 2005). Many studies suggested that the existence of a TFF receptor, is localized at the basolateral cell membrane in epithelial cells, and is exposed only after injuries in the mucosal (Taupin and Podolsky, 2003, Hoffmann, 2009). However, the identity of this receptor is unknown. One study reported that the low-affinity chemokine receptor CXCR4 was identified to be a potential receptor for TFF2 (Dubeykovskaya *et al.*, 2009). As TFF3 are relatively similar to TFF2, it is rational that TFF3 should also be considered as potential ligand for that receptor as well (Hoffmann, 2009). The interaction between TFF3 and a TFF receptor on the membrane of epithelial cells is specific and as a typical binding of ligand-receptor (Yong *et al.*, 2013). The signaling pathways activated by the postulated receptors for TFF on the cell surface to the cytoplasm and/or nucleus remains to be determined. Several studies have proposed that the possible contribution of APC/E-cadherin/ β -catenins, EGF receptors and MAPK as downstream signaling pathways activated by TFF peptides, leading to decreased cell-cell contact and cell-substratum adhesion (Liu *et al.*, 1997, Efstathiou *et al.*, 1998). It has been reported that signaling pathways including Src/RhoA, PI3K/Akt, and phospholipase C/PKC are mediated by TFF peptides to promote cellular invasion and survival of colon carcinoma cells (Emami *et al.*, 2001). Many bioinformatics software are available and can be used to integrate microarray data and *in vitro* experimental data of the functionality of a targeted gene. For

example, DAVID bioinformatics resources is a feasible screening tool for highlighting the functional domain and motif of TFF3 protein, predicting interacting protein to the trefoil domain of TFF3, and integrating the functionality of TFF3 with the downstream signaling pathways. KEGG pathway maps can display the interconnection between TFF3 and the signaling proteins implicated in promoting or inhibiting of tumor growth and progression. The information generated from these tools is required for further validation by *in vitro* and *in vivo* experimental studies. Collaboration researchers from different discipline (bioinformatics and cancer biology) will build up a multi-discipline platform to identify TFF3 interacting proteins on the surface of mammary carcinoma cell lines (Lei *et al.*, 2012). Identification of TFF3 receptor(s) can provide a better understanding of TFF3 biology and develop a novel drug targets for mammary carcinoma progression.

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Appendices

Preparation of buffers

Experiment	Buffers and solutions	Composition
Bacterial Transformation	LB medium	10g Bacto™Tryptone, 5g Bacto™Yeast extract, 5g NaCl, 1L Milli-Q H ₂ O, autoclaved and stored at room temperature
	LB plate	15g agarose was added to 1L liquid LB medium and sterilized by autoclaving. After the medium was cooled down to 50°C, ampicillin was added at the concentration of 100 µg/mL. After gently mixing, the medium was poured into the sterile plates. Upon the medium was solidified, the dishes were stored at 4°C in the inverted position.
Cell culture	RPMI Medium	10.39g/L RPMI powder, 2g/L NaHCO ₄ ; Dissolve it by adding autoclaved H ₂ O, adjust the pH to 7.2 by adding HCl or NaOH, adjust volume to 1L with additional autoclaved H ₂ O and filter sterilize.
	Advanced DMEM-F12	Advanced DMEM-F12 media supplemented with 10 mM L-Glutamine, penicillin/streptomycin and 10% Fetal Bovine Serum
	Complete RPMI medium	450 mL RPMI medium, 50ml heat-inactivated fetal bovine serum, 5mL glutamine, 5mL penicillin/streptomycin
	10x PBS	80g NaCl, 2g KCl, 14.4g Na ₂ HPO ₄ , 2.4g KH ₂ PO ₄ , 1L Milli-Q H ₂ O. Adjust pH to 7.4
	10x trypsin/EDTA solution (0.25%)	2.5g Trypsin, 0.372g EDTA, 0.35g NaHCO ₃ , 1L autoclaved H ₂ O. Adjust pH to 7.2.
	HEPES buffer	0.8766 g NaCl, 0.47688 g HEPES, 100 mL MilliQ H ₂ O. Adjust pH value to 7.4 and sterilize by 0.2 µm filter
	HBSS	0.4g/L Potassium Chloride; 0.06 g/L Potassium Phosphate Monobasic (anhydrous); 8 g/L Sodium Chloride; 0.04788 g/L Sodium Phosphate Dibasic (anhydrous); 1g/L D-Glucose
	Freezing medium	1 mL DMSO, 20 mL heat inactivated fetal bovine serum
	0.4% trypan blue	0.4g Trypan blue, 100 mL 1x PBS.
RNA extraction	DEPC water	1 mL DEPC, 1L Milli-Q H ₂ O. Solution was

		made in the fume hood and stirred overnight at room temperature before being autoclaved.
DNA electrophoresis	50x TAE buffer	242g Tris, 37.2g Na ₂ EDTA.2H ₂ O, 57.2 mL glacial acetic acid, 1L Milli-Q H ₂ O
	10x TBE buffer	108g Tris, 55g boric acid, 7.44g EDTA (pH 8.0), 1 L H ₂ O
	1-2% agarose gel	1-2g agarose, 100 mL 1x TAE buffer or TBE buffer
	1% Ethidium bromide solution	0.2g ethidium bromide, 20 mL Milli-Q H ₂ O
	DNA loading dye 6x	250 mg bromophenol, 30ml glycerol, 70 mL H ₂ O
Protein extraction	Lysis buffer	10 mL (final concentration): 500 µL (1 M Tris-HCl pH 7.4 (121.1 g/mol)); 1 mL (10% Nonidet P-40); 300 µL (5 M NaCl (58.44 g/mol)); 50 µL (0.2 M EDTA (452.24 g/mol)); 1mM NaF; 1mM PMSF; 100 µL (100 mM Na ₃ VO ₄); 1.43 mL (7x protease inhibitor stock); 6.62 mL H ₂ O
SDS-PAGE	4% Stacking gel	500µl 40% acrylamide, 1.26 mL 0.5M Tris-HCl pH 6.8, 50 µL 10% SDS, 3.18 mL Milli-Q H ₂ O, 5 µL TEMED, 25 µL 10% APS
	12% Separating gel	3 mL 40% acrylamide, 2.5 mL 1.5 M Tris-HCl pH 8.8, 100 µL 10% SDS, 4.35 mL Milli-Q H ₂ O, 5 µL TEMED, 50 µL 10% APS
	6x SDS loading dye	6 mL glycerol, 3 mL 1M Tris-HCl, pH 6.8, 1.2g SDS and 5mg bromophenol blue
	1x SDS running buffer	3.03g Tris, 14.41g glycine, 10ml 10% SDS, 1L Milli-Q H ₂ O
	1x Transfer buffer	3.03g Tris, 14.41g glycine, 200 mL MeOH, 800 mL Milli-Q H ₂ O
Western blot	0.1% Tween-20 PBS	100 mL 10x PBS, 900 mL MilliQ H ₂ O, 1 mL Tween-20
	Blocking buffer	5g non-fat dry milk powder, 100 mL 0.1% Tween-20 PBS
	Commassie Blue Stain	2g Commassie Blue; 500 mL MeOH; 70 mL Acetic acid, in 1L H ₂ O
	Commassie destain	95 mL MeOH; 75mL Glacial acetic acid; Made up to 1L with MilliQ H ₂ O
Precast gel Western blot	1x running buffer	1x MOPS SDS buffer (20x) in 600 mL MilliQ H ₂ O
	1X transfer buffer	1x transfer buffer (20x); 10%/20% MeOH; in 500ml MilliQ H ₂ O
BrdU assay	Blocking solution	2% Horse serum in 1x PBS

	Primary Antibody Solution	Anti-BrdU antibody (1:100) in 10 mL PBS with 2% horse serum
	Secondary Antibody Solution	Secondary Antibody (1:200) in 10 mL PBS with 0.2% Triton (2 μ L) and 2% horse serum
	Tertiary Antibody solution	1 drop Reagent A; 1 drop reagent B; 10 mL 1x PBS
	Substrate solution	1 DAB tablet; 1 H ₂ O ₂ tablet; 1 mL MilliQ H ₂ O
Others	1.5 M Tris-HCl	27.3g Tris; 80 mL MilliQ H ₂ O ; Adjust pH value to 8.8 with 2N HCl and make up to 150 mL with MilliQ H ₂ O
	0.5M Tris HCL	9.1 g Tris; 80 mL MilliQ H ₂ O ; Adjust pH value to 6.8 with 2N HCl and make up to 150 mL with MilliQ H ₂ O
	TE buffer	10mM Tris-HCl ; 1mM EDTA pH 8.0
	4x Electrophoresis stock buffer	57.4g Glycine; 7g Tris; 4g SDS; make up to 1L with MilliQ H ₂ O
	Anesthetic for <i>in vivo</i>	10 mL: 1 mL of 100 mg/mL ketamine, 0.5 mL of 2% xylazine and 8.5 mL MilliQ H ₂ O

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